

QY 301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
|||||
Db 7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632
QY 361 GTCTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAACATTGAATATCAG 420
|||||
Db 7633 GTCTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAACATTGAATATCAG 7692
QY 421 TTGACAGAAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCTCTGATAAGCTGTT 480
|||||
Db 7693 TTGACAGAAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCTCTGATAAGCTGTT 7752
QY 481 CTGGTGCAGTACATGCCAAC 501
|||||
Db 7753 CTGGTGCAGTACATGCCAAC 7773

Search completed: April 4, 2003, 06:43:23
Job time : 71.6923 secs

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 566.323 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_7250_7750
Perfect score: 501
Sequence: 1 ttacagggcagtgctttg.....tggtggcagtaacatgcaac 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: en_estba.*

2: en_esthum.*

3: en_estin.*

4: en_estnu.*

5: en_estov.*

6: en_estpl.*

7: en_estro.*

8: en_hic.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_man.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	391	78.0	429	14	N46182
2	230.2	45.9	653	10	AW918387
3	197.4	39.4	3065	11	AK019548
c	196.2	39.2	582	10	BE110717
5	193.2	38.6	699	9	AA124253
6	186.8	37.3	832	13	BI662985

RESULT 1

N46182

LOCUS

DEFINITION

IMAGE:273492 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

N46182 429 bp mRNA linear EST 14-FEB-1996
YV38a07.r1 Soares melanocyte 2NdhM Homo sapiens CDNA clone
IMAGE:273492 5', mRNA sequence.

N46182

IMAGE:273492 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

7 167.6 33.5 324 12 BG002542
c 153.4 30.6 902 9 AI323676
9 148.6 29.7 654 9 AI323285
c 10 141.4 28.2 289 9 AA964962
c 11 140.2 28.0 408 12 BF411653
c 12 128.6 25.7 257 10 AW915133
c 13 120.2 24.0 246 9 AA850189
c 14 109 21.8 483 17 AF310595
c 15 95.2 19.0 634 17 BH290554
c 16 84.2 16.8 753 9 AJ456659
c 17 61.2 12.2 166 10 BE183556
c 18 61.2 12.2 765 13 BI078318
c 19 58.6 11.7 658 13 BM426183
c 20 57 11.4 238 12 BF740733
c 21 43.8 8.7 563 14 BQ394625
c 22 43.6 8.7 240 9 AI441280
c 23 43.2 8.6 647 17 AQ428886
c 24 43.2 8.6 668 13 BM159718
c 25 43.2 8.6 704 13 BM162478
c 26 42 8.4 755 13 BI908180
c 27 41.8 8.3 646 12 BQ33196
c 28 41.6 8.3 987 17 CNS014PQ
c 29 40.8 8.1 523 13 BJ344889
c 30 40.6 8.1 1101 17 CNS001QW
c 31 40.4 8.1 271 10 BS578327
c 32 40.4 8.1 491 9 AI953982
c 33 40.2 8.0 710 17 AQ450260
c 34 40.2 8.0 942 17 CNS00C8A
c 35 40.2 8.0 1023 17 CNS00LA0
c 36 40 8.0 454 9 AI300555
c 37 39.8 7.9 234 9 AL118620
c 38 39.6 7.9 1101 17 CNS017KX
c 39 39.6 7.9 648 17 AZ186649
c 40 39.6 7.9 761 12 BG219214
c 41 39.4 7.9 784 10 BE537207
c 42 39.2 7.8 428 13 BI270529
c 43 39.2 7.8 1100 17 CNS00FSE
c 44 39 7.8 356 9 AL501209
c 45 39 7.8 386 17 AQ953885

ALIGNMENTS

429 bp mRNA linear EST 14-FEB-1996
YV38a07.r1 Soares melanocyte 2NdhM Homo sapiens CDNA clone
IMAGE:273492 5', mRNA sequence.
N46182
IMAGE:273492 5', mRNA sequence.
N46182
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 430.

```

FEATURES
  source
    Location/Qualifiers
      1. .429
        /organism="Homo sapiens"
        /db_xref="GDB:3883134"
        /db_xref="taxon:9606"
        /clone="IMAGE:273492"
        /clone_lib="Soares melanocyte 2NBHM"
        /sex="Male"
        /tissue_type="melanocyte"
        /lab_host="DH10B (ampicillin resistant)"
        /note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGAGTTTCTTTTCTTTTCTTTT
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
      114 a 87 c 91 g 136 t 1 others
BASE COUNT
ORIGIN
  Query Match 78.0%; Score 391; DB 14; Length 429;
  Best Local Similarity 99.3%; Pred. No. 3.3e-65;
  Matches 413; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
  QY 88 AACTCTATTGGAACCAATGACATATGGTTGAATCAACAC-TTTTTTTTTTTT 146
  Db 2 AANTCTATTATGGAACCAATGACATATGGTTGAATCAACAC-TTTTTTTTTT 61
  QY 147 TGTCCTGCTATTCTCATTTGGGTTGCAACAATAATTCATCAAGTAATCATGCCAGCG 206
  Db 62 TGTCCTGCTATTCTCATTTGGGTTGCAACAATAATTCATCAAGTAATCATGCCAGCG 121
  QY 207 ATTATTGATCAAAATCAAAAGGTAATGCACATCCTCATTCACATCAAGCCATGCCA 266
  Db 122 ATTATTGATCAAAATCAAAAGGTAATGCACATCCTCATTCACATCAAGCCATGCCA 181
  QY 267 GGAGACTGGTTTCCCGTGACACATCAATGTCGGAATGAGTGTGCCAGAGTTATTAGT 326
  Db 182 GGAGACTGGTTTCCCGTGACACATCAATGTCGGAATGAGTGTGCCAGAGTTATTAGT 241
  QY 327 GCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGTTGTCATGCTCACTTTTGTGAAGCT 386
  Db 242 GCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGTTGTCATGCTCACTTTTGTGAAGCT 301
  QY 387 GCTCTGCTCAGATCTATCAACATTTGAATATCATGTTGACAGAATGTCGCATGCCGTGGCT 446
  Db 302 GCTCTGCTCAGATCTATCAACATTTGAATATCATGTTGACAGAATGTCGCATGCCGTGGCT 361
  QY 447 -AACATCCTGCTTTGATTCCTCTGATAAGCTGTTCTGTTGGCAGTAACATGCAAC 501
  Db 362 AACATCCTGCTTTGATTCCTCTGATAAGCTGTTCTGTTGGCAGTAACATGCAAC 417
RESULT 2
AW918387 653 bp mRNA linear EST 25-MAY-2000
LOCUS EST349691 Rat gene index, normalized rat, norvegicus, Bento Soares
DEFINITION Rattus norvegicus cDNA clone RCIER58 5' end, mRNA sequence.
ACCESSION AW918387
VERSION AW918387.1 GI:8084163
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 653)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
  Gene Index
  Unpublished (1998)
  Contact: Lee, NH
  The Institute for Genomic Research
  9712, Medical Center Drive, Rockville, MD 20850, USA
  Tel: (301)-838-3529
  Fax: (301)-838-0208
  Email: nhlee@tigr.org
  This clone is available through the ATCC, contact the ATCC
  tel#703-365-2700 for further information
  Seq primer: M13 Reverse.
  Location/Qualifiers
    1. .653
      /organism="Rattus norvegicus"
      /db_xref="taxon:10116"
      /clone="RCIER58"
      /clone_lib="Rat gene index, normalized rat, norvegicus,
Bento Soares"
      /tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
      /lab_host="SOLR"
      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Estimated insert size approx.1 kb"
    180 a 147 c 147 g 179 t
BASE COUNT
ORIGIN
  Query Match 45.9%; Score 230.2; DB 10; Length 653;
  Best Local Similarity 75.9%; Pred. No. 1.4e-34;
  Matches 382; Conservative 0; Mismatches 98; Indels 23; Gaps 7;
  QY 1 TTACAGGCGCAGTCCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGA--GACTTG 58
  Db 70 TTACAGGCGCAGTCCCTTTGTAGCCTATGCTTGTATGGCTCTCTAGTAAATGACTTG 129
  QY 59 AATTAGTTTTTTA-CCTATACCTATGTGAACCTATTATTGGAACCAATGGACATATG 117
  Db 130 AAGTTAGTTTATCTTATCGAGATGTGAACCTGTGTGGAAACCAAGCAGACTCTGG 189
  QY 118 GGTGTTGACTACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCATTTGGGTTGCAAC 177
  Db 190 GTTTGGA-----TTCACTACTGTTGTTCTCTGTGTATCTCTACTGGGATTGCAAC 238
  QY 178 AATAATTCAATCAAGTAATCATGCCAGCGATTATTGATCAAAATCAAAAGTAATGACA 237
  Db 239 ACAATCCGTCAGTAGTCATGCCAGCGAGTAAAT-----CAAGTCGAGCGATGACA 292
  QY 238 TCCTCATCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTG 297
  Db 293 TCCTCATCTAAGCCATG-CTGACCCACAAACCTGGTTTCCCGGTGACACATCCATTG 351
  QY 298 CTGGAATGAGTGTGCCAGAGTTATTAGTCCAGAGTTTTCAGAAAGTTTGAAGCACCAT 357
  Db 352 CTGGAATGAGTGTGCCAGAGTTATTAGTCCAGAGTTCTCTCAGAAAGTCTGAAGCACA- 410
  QY 358 GGTGTGTCATGCTCACTTTTGTGAAAGCTGCTGCTGCTCAGAGTCTATCAACATTTGAATAT 417
  Db 411 AGTATGTCACAAACACTTTTGTGAAACCGCCCTGCTGCTGCT-TGACATCATTAATAT 469
  QY 418 CAGTTGACAGATGGTGCATGCCGTGGGTACATCCCTGTTGATTCCTCTGATAGACT 477
  Db 470 CAGTTGACAAACGGTGCATGCCGTGGGTGACTAAGTCCCATTTTCTCTCTGTAGACT 529
  QY 478 GTTCTGGTGGCAGTAACATGCA 500
  Db 530 GCTGTGTGGCGCTCTTGTGCGA 552
RESULT 3
AK019548 3065 bp mRNA linear HTC 19-JAN-2002
LOCUS AK019548
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4921533C24:ATP-binding cassette, sub-family A
(ABC1), member 1, full insert sequence.

```


[illegible]

QY 297 GCTGGCAATGAGTGTGCCAGAGTTATTAGGCCCAAGTTTTTCAGAAAGTTTGAAGCACCA 356
 Db 375 GCTGGCAATGAGTGTGCCAGAGTTACTAGTGCCCAAGTTGCTCAGAAAGTCTGAAGCA-CT 433
 QY 357 TGGTGTGTCAGTCTCACTTTTGTGAAGCTGCTGCTGCTCAGAGTCTATCAACATTTGAATA 416
 Db 434 GAGTGTGTCACAAACACTTTTGTGAACCCGCCCTACTGCTGCGGT-TGACATCATTAATA 492
 QY 417 TCAGTTGAC-AGAATGCGCATGCGTGGCTAAACATCCTGCTTTGATTCCTC--TGATA 473
 Db 493 TCAGTGCACAAACGCTGCCACATGACTAAATCCCAATTTCTCTCTCTTTGATG 552
 QY 474 AGCTGTTCTGGTGGCAGTAACATGCAA 500
 Db 553 AGCTGCTGTTGCTGCTGCTTGTACAA 579

RESULT 4

LOCUS BEL10717/c
 DEFINITION UI-R-BJ1-avd-f-06-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
 ACCESSION BEL10717
 VERSION 1
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE Rattus.
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized AV canal at 15 dpc library cDNA Library Preparation: M.B. Soares Lab Clone Distribution: clones will be available through Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

Source

1..582
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BJ1-avd-f-06-0-UI"
 /clone_lib="UI-R-BJ1"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pMT3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1 library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Ronaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_LIB=UI-R-BJ1

TAG_TISSUE=AV canal at 15 dpc
 TAG_SEQ=GAAGG*
 BASE COUNT 157 a 129 c 123 g 173 t
 ORIGIN

Query Match 39.2%; Score 196.2; DB 10; Length 582;
 Best Local Similarity 76.9%; Pred. No. 4.6e-28;
 Matches 336; Conservative 0; Mismatches 78; Indels 23; Gaps 7;

QY 1 TTACAGGGGCAGTGCCTTTGTAGCCTATGCTCTTGTATGCTCTCAAGTGAA--GACTTG 58
 Db 434 TTACAGGGGCAGTGCCTTTGTAGCCTATGCTCTTGTATGCTCTCAAGTGAA--GACTTG 58
 QY 59 AATTTAGTTTTTTA-CCTATACCTATGTAAACTCTATTATGGAACCAATGGACATATG 117
 Db 374 AAGTTAGTTTCTATTCTTATGAGATGTAAACTCTGGTGGAAACCAAGCAGACTCTGG 315
 QY 118 GOTTGAACCTACACTTTTTTTTTTTTTTTTTTGTCTGTATCTTCATTTGGGGTTGCAAC 177
 Db 314 GTTTGGA-----TTCATACTGTTTGTCTGTATCTTCATTTGGGGTTGCAAC 266
 QY 178 AATAATCATCAAGTAATCATGCGCAGCGATTATTGATCAAAATCAAAAGTAATGCACA 237
 Db 265 ACAATCCGTCAAGTAGTCATGCGCAGTGATAT-----CAACGTCAAGGCATGTACA 212
 QY 238 TCCTCATCTACTTAAGCCATGCCATGCCAGGAGACTGTTTCCCGGTGACACATCCATTG 297
 Db 211 TCCTCATCTACTTAAGCCATG-CTGACCCACAAACCTGTTTCCCGGTGACACATCCATTG 153
 QY 298 CTGGCAATGAGTGCCTGAGTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCAT 357
 Db 152 CTGGCAATGAGTGCCTGAGTATTAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCAT 94
 QY 358 GGTGTGTCATGCTCACTTTTGTGAAAGCTGCTCTCTCAGAGTCTATCAACATTTGAATAT 417
 Db 93 AGTATGTCACAAACACTTTTGTGAAACCCGCCCTGCTCTCTGT-TGACATCATTAATAT 35
 QY 418 CAGTTGACAGATGGTG 434
 Db 34 CAGGTGACAAACGGGTG 18

RESULT 5

LOCUS AA124253
 DEFINITION mq2198.r1 Barstead MRLB1 Mus musculus cDNA clone IMAGE:579422 5' similar to gp:X75926 M.musculus abcl mRNA (MOUSE);, mRNA sequence.
 ACCESSION AA124253
 VERSION AA124253.1 GI:1682819
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 699)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theissen,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:354070
 Seq primer: -28ml3 rev2 ET from Amersham

FEATURES High quality sequence stop: 506.
Location/Qualifiers
1. .699
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:579422"
/clone_lib="Barstead MFLRB1"
/sex="mixed"
/tissue.type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
/note="Vector: p7N3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5', TGTTACGAATCGAATGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [CATGATTCGGTAC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead."

BASE COUNT 201 a 150 c 156 g 192 t
ORIGIN

Query Match 38.6%; Score 193.2; DB 9; Length 699;
Best Local Similarity 72.8%; Pred. No. 1.6e-27;
Matches 361; Conservative 0; Mismatches 118; Indels 17; Gaps 8;

QY 1 TTACAGGGCAGTCCCTTTAGCTATGCTGTATGGCTCTCAAGTGA--GACTTG 58
Db 215 TTACAGGGCAGTCCCTTTAGCTATGCTGTATGGCTCTCTAGTGAATGACTTG 274

QY 59 AATTAGTTTTTACC-TATACCTATGTGAACTCTATTATGGAACCAATGACATATG 117
Db 275 AAGTTAGTTATTCATACATGATGTGAACCTCTGGTGTGGAACCAACGACATCTGG 334

QY 118 GGTTCGAACTACACATTTTTTTTTTTTTCCTCTGTGATTCATCTATGGGTTGCAAC 177
Db 335 GTTTGGA-----TTCATACCTTTTTTTTTCCTCTGTGATTCATCTAGGATTGCAAC 385

QY 178 AATAAATTCATCAAGTATGCGCCAGGATTTATGATCAAAATCAAAAGTTGAAGCACA 237
Db 386 AACAGTCTATCAATAGTATGCGCCAGTATATCAAAAGTCAAAAGCAGACATCTCTG 445

QY 238 TCC-TCAATCAGTAAAGCCATGCCATGCCAGAGAGACTGGTTCCCGGTGACATCCATT 296
Db 446 TCCATTAAAGCCATTAAAGCCATGCTGAACCAACAAACAGGTTCCCGGTGACATCCATT 505

QY 297 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCAGAGTTTTCAGAAAGTTTGAAGCACA 356
Db 506 CTGGCAATGAGTGTGCGAGAGTATTAGTGCAGAGTTCCTCAGAAAGTCTGAGCA-CT 564

QY 357 TGGTGTGTCATGCTCACTTTTGTGAAGAGTCTCTGCTCAGAGTCTATCAACATTTGAATA 416
Db 565 GAGTGTGTCACCAACACTTTTGTGAAGAGTCTCTGCTCAGAGTCTATCAACATTTGAATA 623

QY 417 TCAGTTGAC-AGATGTCATCGGTGCGTAAACATCTCTGCTGAT-TCCCTCTGATAA 474
Db 624 TCAGTGCACAAAACGGTGGCCATGAGTAAATCCCATTTCCCTTCTCCCTTTGATGA 683

QY 475 GCTGTTCTGTTGCGAG 490
Db 684 GCTGCCGTTGTTGGTGTG 699

RESULT 6
BI662985 832 bp mRNA linear EST 12-SEP-2001
LOCUS 603286357F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5320238 5',
DEFINITION mRNA sequence.
ACCESSION BI662985
VERSION BI662985.1 GI:15577218
KEYWORDS EST.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 832)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1812 row: b column: 15
High quality sequence stop: 809.
Location/Qualifiers
1. .832
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5320238"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue.type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 225 a 185 c 184 g 238 t
ORIGIN

Query Match 37.3%; Score 186.8; DB 13; Length 832;
Best Local Similarity 74.4%; Pred. No. 2.5e-26;
Matches 345; Conservative 0; Mismatches 102; Indels 17; Gaps 8;

QY 1 TTACAGGGCAGTCCCTTTAGCTATGCTGTATGGCTCTCAAGTGA--GACTTG 58
Db 263 TTACAGGGCAGTCCCTTTAGCTATGCTGTATGGCTCTCTAGTGAATGACTTG 322

QY 59 AATTAGTTTTTACC-TATACCTATGTGAACTCTATTATGGAACCAATGACATATG 117
Db 323 AAGTTAGTTATTCATACATGATGTGAACCTCTGGTGTGGAACCAACGACATCTG 381

QY 118 GGTTCGAACTACACATTTTTTTTTTTTTCCTCTGTGATTCATCTAGGTTGCAAC 177
Db 382 GGTTCGATTCATCTATTTTTT-----GTCCCTGTATTCCTCAGGATTGCAAC 432

QY 178 AATAAATTCATCAAGTATGCGCCAGGATTTATGATCAAAATCAAAAGTTGAAGCACA 237
Db 433 AACAGTCTATCAATAGTATGCGCCAGTATATCAAAAGTCAAAAGCAGACATCTCTG 492

QY 238 TCC-TCAATCAGTAAAGCCATGCCATGCCAGAGAGACTGGTTCCCGGTGACATCCATT 296
Db 493 TCATTAAAGCCATTAAAGCCATGCTGAACCAACAAACAGGTTCCCGGTGACATCCATT 552

QY 297 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCAGAGTTTTCAGAAAGTTTGAAGCACA 356
Db 553 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCAGAGTTCCTCAGAAAGTCTGAGCA-CT 611

QY 357 TGGTGTGTCATGCTCACTTTTGTGAAGAGTCTCTGCTCAGAGTCTATCAACATTTGAATA 416
Db 612 GAGTGTGTCACAAACACTTTTGTGAAGAGTCTCTGCTCAGAGTCTATCAACATTTGAATA 670

QY 417 TCAGTTGAC-AGATGTCATCGGTGCGTAAACATCTCTGCTGCTTT 459
Db 671 TCAGTGCACAAAACGGTGGCCATGAGTAAATCCCATTT 714

Db	648	ACAGTTCTTCAAAATAGTATGCCCAAGTATCAAGGTCAAAGGCACACACATCTTCG	589
QY	236	CATCTCATTTACTAAGCCATGCCATGCCCAGGAGACTGGTTCCCGGTGACACATCCAT	295
Db	588	TCATTTAGCCCATTAAGCCATGCTGACCCACANACAGGTTCCCGGTGACACATCCAT	529
QY	296	TGCTGGCAATGAGTGTGCCAGAGTTATTAGTGCCAACTTTTTCAGAAAGTTTGAAGCAC	355
Db	528	TGCTGGCAATGAGTGTGCCAGAGTTACTAGTGCCAACTTGCTCAGANAGTCTGAAGCA-C	470
QY	356	ATGGTGTGTCATGCTCACTTTTGTGAAGTGTGCTGCTCAGAGTCTATCAACATTGAAT	415
Db	469	TGAGTGTGTGCACAAACACTTTTGTGAACACGCCCTACTGCGT-TGACATCAITTAAT	411
QY	416	ATCAGTTGAC-AGAAATGGTGCCATGCGGTGAACATCTGCTTTTGATTCGCTC--TGAT	472
Db	410	ATCAGGTGACAAAACCGTGCCCATGTGATGATAAATCCCATTTTTCCTTCTCTCTTGTGAT	351
QY	473	AAGCTGTTCTGGTGGCAGTAACATGCAA	500
Db	350	GAGTGTGCTGTGTGGCTGTCTTTGTACAA	323

RESULT 9	AI323285	654 bp	mRNA	linear	EST 23-DEC-1998
LOCUS	mq1208.y1	Barstead MFLR1	Mus musculus	cDNA clone	IMAGE:579422.5
DEFINITION	similar to gb:X75926	M.musculus abcl	mRNA (MOUSE);		mRNA sequence.
ACCESSION	AI323285				
VERSION	AI323285.1				
KEYWORDS	GI:4057714				
	EST.				

REFERENCE	ORGANISM	SOURCE	DATE
		house mouse.	
	<i>Mus musculus</i>		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
REFERENCE	1 (bases 1 to 654)		
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lemon, G., Soares, B., Wilton, R. and Waterston, R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousestewatson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:354070
 This read is a RESQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 430.

```

FEATURES
source
1. 654
Location/Qualifiers
    organism="Mus musculus"
    /strain="BALB/c"
    /db_xref="taxon:10090"
    /clone_image:579422"
    /clone_lib="Barstead MPLRBI"
    /sex="mixed"
    /tissue_type="Kidney"
    /dev_stage="6 weeks"
    /lab_host="DH10B"
    /note="vector: pW73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',

```

TGTACGAACTCAAGTGGAGCGCGGCCCTTTTTTTTTTTTTTTTTTTTTT
 341; double-stranded cDNA was ligated to Eco RI adaptors
 [CAGGATTCGGAC], digested with Not I and cloned into the
 Not I and Eco RI sites of the modified pT73 vector.
 Library constructed by Bob Barstead."

BASE COUNT	190 a	144 c	146 g	173 t	1 others
ORIGIN					

Query Match 29.7%; Score 148.6; DB 9; Length 654;
 Best Local Similarity 74.2%; Pred. No. 5.3e-19;
 Matches 253; Conservative 0; Mismatches 74; Indels 16; Gaps 5;

Qy 1 TTACAGGGCAGTGCCTTTTGTAGCTATGCTTCTTATGGCTCTCAAGTAAA--GACTTG 58

Db 221 TTACAGGGCAGTGCCTTTTGTAGCTATGCTTCTTATGGCTCTCTAGTGAAGAAAGACTTG 280

QY	59	AAATTTAGTTTTTACC-TATPACCTATGTGAAACNCTATTATTTGGAACCAATGGACATATG	117
Db	281	AAGTTAGTTCTAATACCTTATACAGATGTGAACCTCTGGTGTGGAACCAAGCAGACTCTGG	340
QY	118	GGTTTGAAGCTCACACTTTTTTTTTTTTTTTTCTCTCTGTATCTTCATTTGGGGTTCGAAC	177

Qy	178	AATTAATTCATCAAGTAATCATGCGCCAGGATATTGA--TCAAAATCAAAAGGTATTGCA	235
Db	392	AACAGTCTCAATATAGTTCATGGCCAGTGATATCAAAAGTCAAAAGGCACACCATCTCT	451
Qy	236	CATCC--TCATTCTACTAAGCCATGCCATGCCCCAGGAGACTGGTTCCCGGTGACACATCC	293
Db	452	CGTCCATTAGCCCTTTAAGCCCTTGCTGAACACACCAACAGGGTTCCGGTGGACACATCC	511
Qy	294	ATTGCTGGCAATGAGTGTGCCAGAGTTATTAGTGCCCAAGTTTTTCAGAA	342
Db	512	ATTGCTGGCCATGAGTGTGCCAGAGTACTAGTGCCTAAGTTGCTCAGAA	560

RESULT 10				
AA964962/c				
LOCUS	AA964962	289 bp	mRNA	linear
DEFINITION	UI-R-C0-hb-c-01-0-VI.s1 UI-R-C0 Rattus norvegicus cDNA clone UI-R-C0-hb-c-01-0-VI 3', mRNA sequence.			
				EST 04-JUL-1999

ACCESSION	AA964962
VERSION	AA964962.1
KEYWORDS	EST.
SOURCE	Norway rat. Rattus norvegicus
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 289)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT On May 18, 1998 this sequence version replaced gi:3138454.

On May 10, 1998 this sequence version replaced g11010101.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult 8-day-embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1773166
Seq primer: M13 Forward
POLYA=No.

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FEATURES
  source
    Location/Qualifiers
      1. .289
        /organism="Rattus norvegicus"
        /strain="Sprague-dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-C0-hb-c-01-0-UI"
        /clone_lib="UI-R-C0"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /note="Vector: pT73D-Pac (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
        library is a subtracted library derived from the UI-R-Al
        and UI-R-E1 libraries. The UI-R-Al library consisted of a
        mixture of individually tagged normalized libraries
        constructed from rat placenta, adult lung, brain, liver,
        kidney, heart, spleen, ovary, and muscle. The UI-R-E1
        library consisted of a mixture of individually tagged
        normalized libraries constructed from 8, 12 and 18-day
        embryo. The tag is a string of 3-5 nucleotides present
        between the Not I site and the oligo-dT track which
        allows identification of the library of origin of a clone
        within the mixture. The subtracted library (UI-R-C0) was
        constructed as follows: PCR amplified cDNA inserts from a
        pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had
        been derived was used as a driver in a hybridization with
        the pooled UI-R-Al and UI-R-E1 library in the form of
        single-stranded circles. The remaining single-stranded
        circles (subtracted library) was purified by
        hydroxyapatite column chromatography, converted to
        double-stranded circles and electroporated into DH10B
        bacteria (Life Technologies) to generate the UI-R-C0
        library. This procedure has been previously described
        (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
        1996)."
      70 a 56 c 67 g 96 t
      BASE COUNT
      ORIGIN
        Query Match 28.2%; Score 141.4; DB 9; Length 289;
        Best Local Similarity 78.6%; Pred. No. 1.7e-17;
        Matches 221; Conservative 0; Mismatches 51; Indels 9; Gaps 4;
      QY 152 CTGTGATTCTCATTGGGTTGCACAAATTAATTCATCAAGTAATCATGCCAGCGATTAT 211
      DB 289 CTGTGATTCTCATTGGGTTGCACAAATTCATCAAGTAATCATGCCAGCGATTAT 230
      QY 212 TGATCAAAATCAAAAGTAATGCATCTCATTCACTAAGCCATGCCATGCCAGGAGA 271
      DB 229 C-----AACGTCGAGGCGATGATCTCCTCATCCATGAAGCCATG-CTGACCCACAAC 177
      QY 272 CTGGTTCCCGGTGACACATCCATTGCTGGCAATGAGTGTGCCAGAGTATTAGTGCCAA 331
      DB 176 CTGGTTCCCGGTGACACATCCATTGCTGGCAATGAGTGTGCCAGATTTATTAGTGCCAA 117
      QY 332 GTTTTCAGAAAGTTGAGCCACCATGGTGTGTCATGCTCATTCTTTTGTGAAGCTGCTCT 391
      DB 116 GTTGCTCAAAAGTCTGAAGCACTA-AGTATGTCACAAACACTTTTGTGAAGACGCCCT 58
      QY 392 GCTCAGAGTCTATCAACATGAATATCATAGTTCACAGAAATGG 432
      DB 57 GCTGCTGT-TGACATCATTAATATCAGGTGACAAACGG 18
      RESULT 11
      BF411653/c
      LOCUS
      DEFINITION
        UI-R-BT1-bmv-a-09-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
        UI-R-BT1-bmv-a-09-0-UI 3', mRNA sequence.
      ACCESSION
        BF411653
      VERSION
        BF411653.1 GI:11399642
      KEYWORDS
        EST.
      SOURCE
        Norway rat.
      ORGANISM
        Rattus norvegicus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
  1 (Bases 1 to 408)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  The sequence contained an oligo-dT track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
  tail. The sequence tag present in the cDNA between the NotI site
  and the oligo-dT track served to identify it as a clone from the
  normalized corpus-striatum library cDNA Library preparation: M.B.
  Soares Lab Clone distribution: clones will be available through
  Research Genetics (www.resgen.com)
  Seq primer: M13 Forward
  POLYA=Yes.
  Location/Qualifiers
    1. .408
      /organism="Rattus norvegicus"
      /strain="Sprague-Dawley"
      /db_xref="taxon:10116"
      /clone="UI-R-BT1-bmv-a-09-0-UI"
      /clone_lib="UI-R-BT1"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies)"
      /note="Vector: pT73D-Pac (Pharmacia) with a modified
      polylinker; Site_1: Not I; Site_2: Eco RI; The library
      UI-R-BT1 is a subtracted library derived from a mixture of
      the following tissues: hippocampus, thalamus, mid-brain,
      medulla, corpus striatum, cerebral cortex and testis. For
      a detailed description of the library from which this
      clone was derived, please visit our web site at
      rated.eng.uiowa.edu. The subtraction has been previously
      described in (Bonaldo, Lennon and Soares, Genome Research
      6:791-806, 1996)
      TAG_LIB=UI-R-BT1
      TAG_TISSUE=corpus-striatum
      TAG_SEQ=CTAGG"
    120 a 82 c 83 g 123 t
    BASE COUNT
    ORIGIN
      Query Match 28.0%; Score 140.2; DB 12; Length 408;
      Best Local Similarity 69.4%; Pred. No. 2.5e-17;
      Matches 284; Conservative 0; Mismatches 103; Indels 22; Gaps 6;
    QY 26 TATGCTGTGATGGCTCTCAAGTGAAG--GACTTGAATTTAGTTTTTA-CCATACCTA 82
    DB 408 TATGCTGTGATGGCTCTATATGATTTAAATGACITGAAGTTAGTTCATTATCTTATGAGA 349
    QY 83 TGTCAAACTCTATTATGGAACCCCAATGGACATATGGGTTTGCACTCACATTTTTTTTT 142
    DB 348 TGTGAAACTCTGGTGTGGACCAACAGCAGATCTGGGTTTGA-----TTCATAC 300
    QY 143 TTTTGTTCCTGTGTATCTCATTTGGGGTTTGGCAACAATAATTCATCAAGTAATCATGGCC 202
    DB 299 TGTGTGTTCTGTGTATTTCTCCTGAGTGAACACAACTCGTCAAGTACTCATGGCC 240
    QY 203 AGCGATTATTGATCAAAATCAAAAGGTAATGACATCTCTCATTCTCATTAGCCCATGCCATG 262
    DB 239 ATTGATAAT-----CAACGTCGAAGGTATCTATCATGTCATCCCTAAGCCCATG-CTGA 187
    QY 263 CCCAGGAGACTGGTTTCCCGGTGACACATCCATTCGTGGCAATGAGTGTGCCAGAGTTAT 322
    DB 186 CCCACAACACTGGTTTCCCGGTGACACATCCCTTGTGGCAATGAGTGTGCCAGATTCAT 127

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QY 323 TAGTGCAAGTTTTCAGAAAGTTTGAAGCACCATTGGTGTGTCATGCTCAGTTTGTGAA 382
|||||
Db 126 TAGTGCAAGTTTTCATGAAAGTCTGAAGCAGTAAAGTATGTCACAAACACATTTTGTGA 67
|||||
QY 383 AGTGTCTGCTCAGAGTCTATCAACATTCGATATGATGAGTTGACAGTAATG 431
|||||
Db 66 AACCGGCATCCTGTTTGT-TGACATCATTAATAATATCAGGTGCGATATG 19
|||||

RESULT 12
AW915133 257 bp mRNA linear EST 25-MAY-2000
LOCUS EST346437 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
DEFINITION RGICJ89 5' end, mRNA sequence.
ACCESSION AW915133
VERSION AW915133.1 GI:8080820
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 257)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
JOURNAL Gene Index
COMMENT Unpublished (1998)
CONTACT: Lee, NH
712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
BASE COUNT 74 a 55 c 53 g 65 t
ORIGIN
FEATURES
source
Location/Qualifiers
1..257
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGICJ89"
/dev_stage="embryo 8, 12, 18 dpc"
/notes="Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"

QY 161 CTCATTGGGTTGCACATAATTTCATCAAGTAATCATGCGCAGCGATTATTGATCAAAA 220
|||||
Db 2 CTCACGTGGATTCCACAAACATCCGTCAGTAGTCATGCGCCAGTATATC-----AA 55
|||||
QY 221 TCAAAAGGTAATGCACATCCTCAATTCACTAAGCCATGCCATGCCAGGAGATGGTTTC 280
|||||
Db 56 CGTCGAGGCATGATACATCCTCATCCACTAAGCCATG-CTGACCCACAAACCTGGTTCC 114
|||||
QY 281 CGGTGACATCATTCGTCGGCAATGAGTGTGCCAGATTATTAGGCCAAGTTTTCAG 340
|||||
Db 115 CGGTGACATCATTCGTCGGCAATGAGTGTGCCAGATTATTAGTGCCCAAGTTGCTCAG 174
|||||
QY 341 AAAGTTTGAAGCACCATTGGTGTGCTGCTCACTTTTGTGAAGCTGCTGCTCAGAGT 400
|||||
Db 175 AAAGTCTGAGGCACTA-AGTATGTCACAAACATTTTGTGAAGCAGCCGCTGCTGCTGT 233
|||||
QY 401 CTATCAACATTTGAATATCAGTTGAC 425
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Db 234 -TGACATCATTAATAATATCAGGTGAC 257
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RESULT 13
AA850189 246 bp mRNA linear EST 30-APR-1998
LOCUS EST192956 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVAD66 3' end, mRNA sequence.
ACCESSION AA850189
VERSION AA850189.1 GI:2937729
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 246)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
JOURNAL Gene Index
COMMENT Unpublished (1998)
CONTACT: Lee, NH
712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
BASE COUNT 63 a 50 c 61 g 72 t
ORIGIN
FEATURES
source
Location/Qualifiers
1..246
/organism="Rattus sp."
/db_xref="ATCC (inhost):2008662"
/db_xref="taxon:10118"
/clone="ROVAD66"
/notes="Normalized rat ovary, Bento Soares"
/notes="Organ: ovary; Vector: pT73pac; Site_1: EcoRI;
Site_2: NotI"

QY 169 GGTTCGCAACAATAATTCATCAAGTAATCATGCGCAGCGATTATTGATCAAAAATCAAAAGG 228
|||||
Db 246 GATTGCAACAACAATCCGTCAGTAGTCATGCGCCAGTATAT-----CAACGTCGAAG 193
|||||
QY 229 TAATGCACATCTCATTCATCAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACA 288
|||||
Db 192 GCATGTACATCTCATCTCCACTAAGCCATGCTGA-CCCAAAACCTGGTTCCCGGTGACA 134
|||||
QY 289 CATCCATTGCTGCAATGAGTGTGCCAGATTATTAGTGCCCAAGTTTTCAGAAAGTTTG 348
|||||
Db 133 CATCCATTGCTGCAATGAGTGTGCCAGATTATTAGTGCCCAAGTTTTCAGAAAGTTTG 74
|||||
QY 349 AAGCACCATTGGTGTGCTGCTCACTTTTGTGAAGAGTCTGCTGCTCAGAGTCTATCAAC 408
|||||
Db 73 AAGCACTA-AGTATGTCACAAACACTTTTGTGAAGCAGCCGCTGCTGCTGT-TGACATC 16
|||||
QY 409 ATTGATATCAGTTG 423
|||||
Db 15 ATTAATATCAGGTG 1
|||||

RESULT 14
AZ310595 483 bp DNA linear GSS 29-SEP-2000
LOCUS IM0025E11R Mouse 10kb plasmid U9GCM library Mus musculus genomic
DEFINITION clone U9GCM0025E11 R, DNA sequence.
ACCESSION AZ310595
VERSION AZ310595.1 GI:10352738
KEYWORDS GSS.
SOURCE house mouse.
```

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 483)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: E column: 11
Seq primer: CACACAGGAAACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 483.
FEATURES
    source
    1..483
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGCLM0025E11"
        /clone_lib="Mouse 10kb plasmid UUGCLM library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /note="Vector: PWD42hv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (g14732114[g147129072.1]), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
BASE COUNT      138 a 110 c 96 g 139 t
ORIGIN
Query Match      21.8%; Score 109; DB 17; Length 483;
Best Local Similarity 77.6%; Pred. No. 2.2e-11;
Matches 201; Conservative 0; Mismatches 40; Indels 18; Gaps 5;
QY 1 TTACAGGGCAGTGGCTTTGTAGCTATGCTGTGTATGGCTCTCAAGTGAAA--GACATTG 58
DB 244 TTACAGGGCAGTGGCTTTGTAGCTATGCTGTGTATGGCTCTCAAGTGAAAATGACATTG 185
QY 59 AATTAGTTTTTACC-TATACCTAGTGAAACTCTATTATGGAAACCAATGACATATG 117
DB 184 AAGTAGTTCATTACCTTATACAGATGTGAAACTCTGGTGGTGAACCAAGCAGAC-TCGTG 126
QY 118 GGTTCGACTACACTTTTTTTTTTTTGTCTGCTGTATTCATCTGGGTTGCAAC 177
DB 125 GGTTCGACTACAC-----TTTTTTGTCTGCTGTATTCATCTAGATGTCAC 74
QY 178 AATAATTCATCAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGTAAATGCACA 237

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Db 73 AACAGTCTATCAATAGTCATGGCCAGTGATAAT-----CAAAGTCAAAGGCACACACA 20
QY 238 TCCTCATTCCTAAGCCAT 256
Db 19 TCCTCGTCCATTAAAGCCAT 1
RESULT 15
BH290554      634 bp DNA linear GSS 30-NOV-2001
LOCUS      CH230-78A16.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
DEFINITION      CH230-78A16, DNA sequence.
ACCESSION      BH290554
VERSION      BH290554.1 GI:17202962
KEYWORDS      GSS.
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 634)
AUTHORS      Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-78A16.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or erling_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 78 row: A column: 16
Seq primer: SP6
Class: BAC ends.
FEATURES
    source
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QY 118 GGTTCGACTACACTTTTTTTTTTTTGTCTGCTGTATTCATCTGGGTTGCAAC 177
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Search completed: April 3, 2003, 16:37:00
Job time : 572.323 secs

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 1539.86 Seconds
(without alignments)
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: gb_pl.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	773	99.5	3366	6	AX060897	Sequence
3	773	99.5	10442	6	AX060713	Sequence
4	773	99.5	10442	6	AX060892	Sequence
5	773	99.5	10442	9	AF285167	Homo sapi
6	773	99.5	10474	6	AX060719	Sequence
7	773	99.5	10474	6	AX060721	Sequence
8	773	99.5	10474	6	AX060898	Sequence
9	773	99.5	10474	6	AX060900	Sequence
10	688	88.5	149034	9	AF275948	Homo sapi
11	688	88.5	182012	9	AL359846	Human DNA
12	688	88.5	201144	9	AF287262	Homo sapi
13	673	86.6	183999	9	AX092589	Sequence
14	666	85.7	3501	6	AX059896	Sequence
15	666	85.7	5352	6	AX127778	Sequence
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AUTHORS	AX060718.1	Sequence	6	from Patent WO0078972.	3366 bp	DNA	linear	PAT 22-JAN-2001
TITLE	AX060718.1	Sequence	6	from Patent WO0078972.	3366 bp	DNA	linear	PAT 22-JAN-2001
JOURNAL	AX060718.1	Sequence	6	from Patent WO0078972.	3366 bp	DNA	linear	PAT 22-JAN-2001

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 /db_xref="taxon:9606"

BASE COUNT 1119 a 564 c 559 g 1120 t 4 others
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 Best Local Similarity 100.0%; Pred. No. 6.9e-142;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 721 ACAACAGATTTCTAGTTAAATCAATTTTCAATTAAGGAAAGAAAAAATTTT 777
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 DEFINITION Sequence 6 from Patent WO0078971.
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 VERSION AX060897.1 GI:12406274
 KEYWORDS human.
 SOURCE

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3366)
 AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
 TITLE Atp binding cassette transporter protein abcl polypeptides
 JOURNAL Patent: WO 0078971-A 6 28-DEC-2000;
 CV THERAPEUTICS, INC. (US)
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DEFINITION Sequence 1 from Patent WO0078972.
ACCESSION AX060713
VERSION AX060713.1 GI:12406103
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Law, R.M., Wade, D., and Garvin, M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX060892 10442 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078971.
ACCESSION AX060892
VERSION AX060892.1 GI:12406270
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10442)
AUTHORS Law, R.M., Wade, D., Oram, J.F., and Garvin, M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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RESULT 5
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 LOCUS Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
 DEFINITION complete cds.
 ACCESSION AF285167
 VERSION AF285167.1 GI:9755158
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10442)
 AUTHORS Schwartz,K., Lawn,R.M. and Wade,D.P.
 TITLE ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 10442)
 AUTHORS Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K., Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc., 3172 Porter Drive, Palo Alto, CA 94304, USA

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 BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
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 Best Local Similarity 100.0%; Pred. No. 5.5e-142;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 9920 GTCATGTAATGTAACCCCTTTGATATTGAGACATTAATTTGGACCTTGGTATTATCTA 9979
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LOCUS Sequence 7 from Patent WO0078972.
DEFINITION AX060719
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 AAAACACCAAACTCAGACTACTGTATTTTCATTTATCTGTACTGAAGCAAAATGCTTTG 300
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QY 301 TGACTATTAATGTGTGCACATCATTCCTACTGTATAGTAATCATTTGACTAAAGCCATT 360
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Db 9832 TGACTATTAATGTGTGCACATCATTCCTACTGTATAGTAATCATTTGACTAAAGCCATT 9891
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QY 361 TCGTGTGTTTCTTCTGTGNTGNATATATCAGGTAATAATTTTCCAAAGAGCCATGT 420
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Db 9892 TCGTGTGTTTCTTCTGTGNTGNATATATCAGGTAATAATTTTCCAAAGAGCCATGT 9951
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QY 421 GTCATGTAATCTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA 480
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Db 10252 ACAACAGATTTCTAAGTAAATCATTTTCAATTAAGAGGAAAAAGAAAAAATTTT 10308
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RESULT 7
AX060721 AX060721 10474 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 9 from Patent WO0078972.
DEFINITION AX060721
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 60
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Db 9532 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 9591
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QY 61 TATATCCCTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 120
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Db 9592 TATATCCCTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 9651
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QY 121 AATTTCGCTTTTGCATCTTTGGACACCTCAGAAAATTTTAAACACCTGTGAATATGA 180
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Db 9652 AATTTCGCTTTTGCATCTTTGGACACCTCAGAAAATTTTAAACACCTGTGAATATGA 9711
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QY 181 GAAATACAGAGAAAAATAAAGCCCTCTATACATAATGCCAGCAAAATTTCAATTTGTA 240
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QY 241 AAAACACCAAACTCAGACTACTGTATTTTCATTTATCTGTACTGAAGCAAAATGCTTTG 300
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Db 9772 AAAACACCAAACTCAGACTACTGTATTTTCATTTATCTGTACTGAAGCAAAATGCTTTG 9831
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QY 301 TGACTATTAATGTGTGCACATCATTCCTACTGTATAGTAATCATTTGACTAAAGCCATT 360
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Db 9892 TCGTGTGTTTCTTCTGTGNTGNATATATCAGGTAATAATTTTCCAAAGAGCCATGT 9951
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QY 421 GTCATGTAATCTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA 480
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QY 661 GTAATGGATCTATTTTGCATGGAATATCTGAGAAATTCGAAAGTTCGAAAGTTC 720
Db 10192 GTAATGGATCTATTTTGCATGGAATATCTGAGAAATTCGAAAGTTCGAAAGTTC 10251
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Db 10252 ACAACAGATTTCTAAGTTAAATCATTTTCAATTAAGGAAAAAGAAAAATTTT 10308

RESULT 8
AX060898
LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078971.
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 9532 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9591
QY 61 TATATCCCTGTGGAATGATACCTATGTGAGTTTCAGAAATTCGAAATACGTTTCAA 120
Db 9592 TATATCCCTGTGGAATGATACCTATGTGAGTTTCAGAAATTCGAAATACGTTTCAA 9651
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACTGTGAATATGA 180
Db 9652 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACTGTGAATATGA 9711
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QY 301 TGACTATTAAATGTTGCACATCATTCATCTAGTATAGTATCATTTGACTAAAGCCATT 360
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QY 361 TCGTGTGTTTTCTTCTGTGGTGNATATATCAGGTAATATTTTCCAAAGGCAATGT 420

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RESULT 9
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LOCUS AX060900 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078971.
ACCESSION AX060900
VERSION AX060900.1 GI:12406276
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
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QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACTGTGAATATGA 180
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QY 181 GAAATACAGAAATAATAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 240
Db 9712 GAAATACAGAAATAATAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 9771
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QY	421	GTCAATGTAATACGAAACCCCTTTCATATTCAGACATTAATTTGGACCCCTTGGTATTATCTA	480
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QY	541	TTAAANGTCTATTTCCATAAGGATTTAGCTTGCTTATCCCTTCTATACCTTAAGATG	600
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DEFINITION	AF275948		
ACCESSION	AF275948		
VERSION	AF275948.1	GI:9247085	
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
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AUTHORS			
TITLE			
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FEATURES			
source			
gene			
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Db 147927 AATTT 147932

LOCUS

VERSION

SOURCE
ORCA.HTT.COM

REFERENCE AUTHORS

JOURNAL

FEATURES

source

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[illegible]

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Query Match      88.5%; Score 688; DB 9; Length 182012;
Best Local Similarity 97.1%; Pred. No. 1.4e-125;
Matches 763; Conservative 0; Mismatches 14; Indels 9; Gaps 6;

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QY 61 TATATTCCTGTGGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTTCAA 120
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Db 178551 TATATTCCTGTGGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTTCAA 178492
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Db 178491 AATTTCTGCTTTTGCACTTTTGGGACACCTCAGAAAACCTTATTAACAACCTGTGAATATGA 178432
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Db 178431 GAAATACACAAGAAATATAAAGCCCTCTATACATAAATGCCACACAAATTCATTTGTTA 178372
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Db 178371 AAAACAACCAACCACTACACTACTGTATTTTCATTTATCTGTAAGGCAAAATTCCTTTG 178312
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Db 178311 TGACTATTAAATGTTGGACATCACTTCACTGTATAGTAAATTCATTCATTAAGGCCAAT 178252
QY 361 TG-CTGTGTTTTCTTCTTGTGNGTGNATATATCAGGTAAATATTTTCCAAAGAGCCCATG 419
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Db 178251 TGCTGTGTTTTCTTCTTGTGNGTGNATATATCAGGTAAATATTTTCCAAAGAGCCCATG 178192
QY 420 TGCTGTGTTTTCTTCTTGTGNGTGNATATATCAGGTAAATATTTTCCAAAGAGCCCATG 478
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Db 178191 TGCTGTGTTTTCTTCTTGTGNGTGNATATATCAGGTAAATATTTTCCAAAGAGCCCATG 178132
QY 479 TACTAG-AATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 535
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QY 536 CCCCCTTAAAANG-TTCTATTTCCTAAGGATTTAGCT---TGCTTATCCCTTCTTATATC 591
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Db 178071 CCCCCTTAAAANG-TTCTATTTCCTAAGGATTTAGGATTTAGGATTTAGGATTTAGGATTTAGGATTT 178012
QY 592 CTTAGATGAACTGTTTTTGTGCTTTTGTTCATCATCTGCGCCCTCATTCGACGACATTT 651
|||||
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QY 652 ACGTGTCTGTAATGGGATCTATTTTGCATGGAATATCTGAGAATTCGAAAATCTAGAC 711
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QY 712 AAAAGTTTCAACAAGAGATTTCTAAGTAAATCATTTTCATTAAGGAAAAAGAAAAA 771
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RESULT 12
LOCUS AF287262
DEFINITION Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1)
and SNAP protein genes, complete cds.
ACCESSION AF287262
VERSION AF287262.1 GI:13876612
KEYWORDS SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201144)
Qiu, X., Cavellier, L., Chiu, S., Yang, X., Rubin, E. and Cheng, J.F.
Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
JOURNAL MEDLINE
PUBMED 21251004
11352567
REFERENCE 2 (bases 1 to 201144)
AUTHORS Qiu, X., Cavellier, L., Chiu, S., Rubin, E. and Cheng, J.-F.
TITLE Direct Submission

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JOURNAL Submitted (13-JUL-2000) Genome Science Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley, CA 94720, USA

FEATURES

source Location/Qualifiers

1. .201144

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organism="Homo sapiens"

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exon

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Query Match 88.5%; Score 688; DB 9; Length 201144;
Best Local Similarity 97.1%; Pred. No. 1.4e-125;
Matches 763; Conservative 0; Mismatches 14; Indels 9; Gaps 6;

QY 1 GTAAACCTAATTGTGGTAGAAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG 60
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Db 181187 TATATTCCTGTGGATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTGTTCAA 181246
QY 121 AATTTCTGCTTTTGGACACCTTGGGACACCTCAGAAACTTATTAACAACCTGGAATATGA 180
Db 181247 AATTTCTGCTTTTGGACACCTTGGGACACCTCAGAAACTTATTAACAACCTGGAATATGA 181306
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Db 181307 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 181366
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Db 181367 AAAACAACCAACCTCAGACCTGATTTTCAATATCTGCTACTGAAAGCAAAATGCTTTG 181426
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Db 181487 TGCTGTGTTTCTTCTTGTGGTGTATATATCATTCAGTAAATATTTTCCAAAGCCCATG 181546
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QY 772 AATTTT 777
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LOCUS AX092589 183999 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0115676.
ACCESSION AX092589
VERSION AX092589.1 GI:13444647
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183999)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
triglyceride levels
JOURNAL Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES
source
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/db_xref="taxon:9606"
BASE COUNT 49549 a 37944 c 41170 g 54950 t 386 others
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Query Match 86.8%; Score 673; DB 6; Length 183999;
Best Local Similarity 95.7%; Pred. No. 1.2e-122;
Matches 753; Conservative 10; Mismatches 14; Indels 10; Gaps 7;

QY 1 GTAAACCTAATTGTGGTAGAAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG 60
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QY 121 AATTTCTGCTTTTGGACACCTTGGGACACCTCAGAAACTTATTAACAACCTGGAATATGA 180
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QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
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QY 241 AAAACAACCAACCTCAGACCTGATTTTCAATATCTGCTACTGAAAGCAAAATGCTTTG 300
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QY 771 AAATTTT 777
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RESULT 14
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LOCUS AX059896 3501 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 14 from Patent WO0078970.
ACCESSION AX059896
VERSION AX059896.1 GI:12405554
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.
Nucleic and proteinic acids corresponding to human gene abcl
Patent: WO 0078970-A 14 28-DEC-2000;
Aventis Pharma S.A. (FR)
FEATURES
Location/Qualifiers
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Query Match 85.7%; Score 666; DB 6; Length 3501;
Best Local Similarity 96.8%; Pred. No. 6.2e-121;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;
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QY 241 AAAAACACCAACCAACCTCACACTACTGTTTCAATTCATCTGTAAGTGAAGCAATGTTTG 300
Db 1147 AAAAACACCAACCAACCTCACACTACTGTTTCAATTCATCTGTAAGTGAAGCAATGTTTG 1206
QY 301 TGACTATTAATGTTGACATCATTCATTCACGTGATAGTAATCATTCAGTAAAGCCATT 360
Db 1207 TGACTATTAATGTTGACATCATTCATTCACGTGATAGTAATCATTCAGTAAAGCCATT 1266
QY 361 TG-CTGTGTTTCTTGTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 419
Db 1267 TGTCTGTGTTTCTTGTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 1326
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Db 1327 TGTCTATGTAATACAGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTGTTATTC 1386
QY 478 CTACTAG-AATAAGTAAATACAGAACCTTATTCGCTCTAATTTT--CAAAATGTTGCA 534
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QY 770 AAATTTT 777
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RESULT 15
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LOCUS AX127778 5352 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 17 from Patent WO0130848.
ACCESSION AX127778
VERSION AX127778.1 GI:14134425
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 17 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
Location/Qualifiers
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QY	241	AAAACCAACCAACCTCACACTACTGTATTTTCTATCTCTGTAAGCAAAATTCGTTG	300		
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DB	3058	TGACTATTAATGTGCACATCATTCATTCACCTGATAGTATTAATGACTAAAGCCATT	3117		
QY	361	TG-CTGTTTCTCTGTTGGTGNATATATCAGGTAAATAATTTTCCAAAGAGCCATG	419		
DB	3118	TGCTGTGTTTCTCTGTTGGTGNATATATCAGGTAAATAATTTTCCAAAGAGCCATG	3177		
QY	420	TGTCATGTAATCTGAACC-CTTTGATATGAGACATTAATTTGGACCT-TGSTATAT	477		
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DB	3358	CCCTAAGATGAAGCTGTTTGTGCTCTTTGTTTCATCATTTGGCCCTCATTCCAAGCACTT	3417		
QY	651	TACGCTGTCGTAATGGGATCTATTTTGCACCTGGAATATCTCAGAAATTCAGAACTAGA	710		
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GenCore version 5.1.4_p5_4578
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Scoring table: IDENTITY_NUC

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	773	99.5	3366	22 AAF24706	Nucleotide sequenc
3	773	99.5	10442	22 AAF24680	Nucleotide sequenc
4	773	99.5	10442	22 AAF24702	Nucleotide sequenc
5	773	99.5	10474	22 AAF24685	Nucleotide sequenc
6	773	99.5	10474	22 AAF24686	Nucleotide sequenc
7	773	99.5	10474	22 AAF24707	Nucleotide sequenc
8	773	99.5	10474	22 AAF24708	Nucleotide sequenc
9	673	86.6	183999	22 AAF92831	Human ABC1 genomic

10 666 85.7 5352 22 AAS04049 Human ABC1 gene, p
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14 427.2 55.0 554 22 AAH13302 Human cDNA clone (
15 331 42.6 9741 22 AAS06120 Human ABC1 DNA seq
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19 327 42.1 451 24 ABL64032 Breast cancer rela
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21 110 14.2 210 16 AAT22245 Human gene signatu
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23 46.6 6.0 7195 22 AAS43324 Chemically pretrea
24 46.6 6.0 7195 24 ABK28165 DNA transcription
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26 45.6 5.9 5457 24 ABL33131 Human immune syste
27 45.6 5.9 5986 24 AAS61432 Human gene regulat
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43 43.2 5.6 103929 21 AAF22287 BAC containing rep
44 42.6 5.5 154902 24 ABQ88198 Human osteoblast d
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ALIGNMENTS

RESULT 1
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ID AAF24684 standard; DNA; 3366 BP.

XX AC AAF24684;

XX DT 20-APR-2001 (first entry)

XX DE Nucleotide sequence of the 3' flanking region of the human ABC1 gene.

XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

XX KW chromosome 9q22-q31; heart disease; hypercholesterolemia;

XX KW atherosclerosis; cholesterol transport; ss.

XX OS Homo sapiens.

XX PN WO200078972-A2.

XX PD 28-DEC-2000.

XX PF 16-JUN-2000; 2000WO-US16765.

XX PR 18-JUN-1999; 99US-0140264.

XX PR 14-SEP-1999; 99US-0153872.

XX PR 19-NOV-1999; 99US-0166573.

XX PA (CVTH-) CV THERAPEUTICS INC.

XX PI Lawn RM, Wade D, Garvin M;

XX WPI; 2001-137812/14.

XX DR

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 146-148; 215pp; English.
XX
CC The present sequence represents the 3' flanking region of the human
CC adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
CC resides in cell membranes and utilizes ATP hydrolysis to transport a wide
CC variety of substrates across the plasma membrane. ABC1 is a pivotal
CC protein in the apolipoprotein-mediated mobilisation of intracellular
CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic
CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
CC gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
CC are useful for developing pharmaceutical agents for the treatment of
CC heart disease and other disorders associated with hypercholesterolemia
CC and atherosclerosis. The genes are useful for developing screening assays
CC to screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 3366;
Best Local Similarity 100.0%; Pred. No. 8.3e-165;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TATATCCCTGTTGGAATGATACCTATGAGTTTCAGAAATTTCTCAAAATACGTTTCAA 120
DB 2484 TATATCCCTGTTGGAATGATACCTATGAGTTTCAGAAATTTCTCAAAATACGTTTCAA 2543

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DB 2544 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAACAACGTGGAATAGA 2603

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DB 2664 AAAAACAACCAACCTCACACTACTGTTATTCATATCTGCTACTGAAACAATGCTTTG 2723

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DB 2724 TGACTATTAAATGTTGCATCATTCATTCACCTGATATAGTATATCATTCAGTAAAGCCATT 2783

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ID AAF24706 standard; DNA; 3366 BP.
XX
AC AAF24706;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of the 3' flanking region of the human ABC1 gene.
XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX
OS Homo sapiens.
XX
PN WO200078971-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16591.
XX
PR 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX
PA (CVTH-) CV THERAPEUTICS INC.
PA (UNIW) UNIV WASHINGTON.
XX
PI Lawn RM, Wade D, Oram JF, Garvin M;
XX
DR WPI; 2001-137811/14.
XX
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 142-144; 211pp; English.

XX The present sequence represents the 3' flanking region of the human
XX adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
XX resides in cell membranes and utilizes ATP hydrolysis to transport a wide
XX variety of substrates across the plasma membrane. ABC1 is a pivotal
XX protein in the apolipoprotein-mediated mobilisation of intracellular
XX cholesterol stores. ABC1 is defective in Tangier disease, a genetic
XX disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
XX gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
XX are useful for developing pharmaceutical agents for the treatment of
XX heart disease and other disorders associated with hypercholesterolemia
XX and atherosclerosis. The genes are useful for developing screening assays
XX to screen for compounds that regulate the expression of genes associated
XX with cholesterol transport. The genes and proteins are also useful for
XX are also useful as diagnostic indicators of cardiovascular disease and
XX other disorders associated with hypercholesterolemia.
XX
SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 3366;
Best Local Similarity 100.0%; Pred. No. 8.3e-165;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTAAACCTAATGTGGTAGAAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2424 GTAAACCTAATGTGGTAGAAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2483
QY 61 TATATTCCTGTGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 120
DB 2484 TATATTCCTGTGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 2543
QY 121 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACTATGAATGA 180
DB 2544 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACTATGAATGA 2603
QY 181 GAAATACAGAGAAAATTAATAAGCCCTCTATACATAAATGCCAGACATTCATTGTTA 240
DB 2604 GAAATACAGAGAAAATTAATAAGCCCTCTATACATAAATGCCAGACATTCATTGTTA 2663
QY 241 AAAAACAACCAACCTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTG 300
DB 2664 AAAAACAACCAACCTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTG 2723
QY 301 TGACTATTAATGTGACATCAATTCATTACCTGATAGTAATCATGTAGTAAGCCATT 360
DB 2724 TGACTATTAATGTGACATCAATTCATTACCTGATAGTAATCATGTAGTAAGCCATT 2783
QY 361 TGCTGTGTTTCTTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGAGCCATGT 420
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QY 481 CTAGAAATATGTAATCTAGTGNAGAAATATGCTCTAATCTTTCAAAATGTGCATCCCC 540
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QY 541 TTAAGNGTCTAATTTCCATGAAGATTTAGCTGCTTATCCCTTCTTATACCCCTAGATG 600
DB 2964 TTAAGNGTCTAATTTCCATGAAGATTTAGCTGCTTATCCCTTCTTATACCCCTAGATG 3023
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QY 721 ACAACAGATTTCTAAGTTAAATCATTTTCAATTAAGGAAAAAGAAAAAATTTT 777
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RESULT 3
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ID AAF24680 standard; DNA; 10442 BP.
XX AC AAF24680;
XX DT 20-APR-2001 (first entry)
XX DE Nucleotide sequence of a human ABC1 polypeptide.
XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
XX KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
XX KW atherosclerosis; cholesterol transport; ss.
XX OS Homo sapiens.
XX PH Key
XX FT CDS
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FT XX /product= "ABC1 polypeptide"
PN XX WO200078972-A2.
XX XX 28-DEC-2000.
XX XX 16-JUN-2000; 2000WO-US16765.
XX XX 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX (CVTH-) CV THERAPEUTICS INC.
XX XX Lawn RM, Wade D, Garvin M;
XX WPI; 2001-137812/14.
XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX Disclosure; Page 122-128; 215pp; English.
XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
XX Query Match 99.5%; Score 773; DB 22; Length 10442;
XX Best Local Similarity 100.0%; Pred. No. 1e-164;
XX Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 9620 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACTATGAATGA 9679
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QY 241 AAAAACAACCAACCTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTG 300
DB 9740 AAAAACAACCAACCTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTG 9799
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RESULT 4

AAF24702
 ID AAF24702 standard; DNA; 10442 BP.
 AC AAF24702;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of a human ABC1 polypeptide.
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;
 KW apolipoprotein-mediated mobilisation; cholesterol; tangier disease;
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 291..7076
 FT /tag- a
 FT /product= "ABC1 polypeptide"
 XX
 PN WO200078971-A2.
 XX
 XX 28-DEC-2000.
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 PF 16-JUN-2000; 2000WO-US16591.
 XX
 PR 18-JUN-1999; 99US-0140264.
 PR 14-SEP-1999; 99US-0153872.
 PR 19-NOV-1999; 99US-0166573.
 XX
 PA (CVTH-) CV THERAPEUTICS INC.
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Lawn RM, Wade D, Oram JF, Garvin M;
 XX
 WIPI: 2001-137811/14.
 DR P-PSDB; AAB31365.
 XX
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX
 PS Claim 3; Page 117-123; 211pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
 CC membranes and utilises ATP hydrolysis to transport a wide variety of
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
 CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
 CC useful for developing pharmaceutical agents for the treatment of heart
 CC disease and other disorders associated with hypercholesterolemia and
 CC atherosclerosis. The genes are useful for developing screening assays to
 CC screen for compounds that regulate the expression of genes associated
 CC with cholesterol transport. The genes and proteins are also useful for
 CC are also useful as diagnostic indicators of cardiovascular disease and
 CC other disorders associated with hypercholesterolemia.

XX SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 10442;
 Best Local Similarity 100.0%; Pred. No. 1e-164;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTGAAGAAATTTTACCACACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 9500 GTAAACCTAATTTGGTGAAGAAATTTTACCACACTCTATCTCAATCAAGCAAAATTTCTG 9559
 QY 61 TATATTCCTCTGGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATAGCTGTTCAAA 120
 Db 9560 TATATTCCTCTGGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATAGCTGTTCAAA 9619
 QY 121 AATTTCTGCTTTTGCAATCTTTGGGACACCTCAGAAACTTATTAACTGCTGAATATGA 180
 Db 9620 AATTTCTGCTTTTGCAATCTTTGGGACACCTCAGAAACTTATTAACTGCTGAATATGA 9679
 QY 181 GAATACAGAGAAATTAATAGCCCTCTATACATTAATGCCAGCACATTCATCTGTTA 240
 Db 9680 GAATACAGAGAAATTAATAGCCCTCTATACATTAATGCCAGCACATTCATCTGTTA 9739
 QY 241 AAAACAAACCAACCTCACACTACTGTATTTTCTATCTGTAAGCAAAATGCTTTG 300
 Db 9740 AAAACAAACCAACCTCACACTACTGTATTTTCTATCTGTAAGCAAAATGCTTTG 9799
 QY 301 TGACTATTAAATGTTGCACATCATCTTCACTGTATAGTAAATCATTCAGTAAAGCCATT 360
 Db 9800 TGACTATTAAATGTTGCACATCATCTTCACTGTATAGTAAATCATTCAGTAAAGCCATT 9859
 QY 361 TGCTGTGTTTTCTTCTTGTGNTGNATATATATATATATATATATATATATATATATATAT 420
 Db 9860 TGCTGTGTTTTCTTCTTGTGNTGNATATATATATATATATATATATATATATATATAT 9919
 QY 421 GTCATGTAATACCTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA 480
 Db 9920 GTCATGTAATACCTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA 9979
 QY 481 CTAGAATAATGTAATCTACTGNAGAAATATTGCTCTAATTTCTTTCAAAATGGTGCATCCCC 540
 Db 9980 CTAGAATAATGTAATCTACTGNAGAAATATTGCTCTAATTTCTTTCAAAATGGTGCATCCCC 10039
 QY 541 TTTAAANGTTCTATTTCCTAAGATTTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG 600
 Db 10040 TTTAAANGTTCTATTTCCTAAGATTTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG 10099
 QY 601 AAGCTGTTTTTGGCTTTGTTTCATCTGCGCCCTCATTCGACGACATTTACGCTGTCT 660
 Db 10100 AAGCTGTTTTTGGCTTTGTTTCATCTGCGCCCTCATTCGACGACATTTACGCTGTCT 10159
 QY 661 GTAATGGATCTATTTTGGCACTGGAATATCTGAGAAATTCGAAAACTAGACAAAAGTTTC 720
 Db 10160 GTAATGGATCTATTTTGGCACTGGAATATCTGAGAAATTCGAAAACTAGACAAAAGTTTC 10219
 QY 721 ACAACAGATTTCTAAGTTAAATCATTTTCAATTAAGGAAAGAAAGAAATTTT 777

Db 10220 ACAACAGATTCTAAGTAAATCAATTTTCATTAAAGGAGAAAGAAAAAATTTT 10276

RESULT 5

AAF24685

ID AAF24685 standard; DNA; 10474 BP.

XX AAF24685;

AC AAF24685;

XX 20-APR-2001 (first entry)

DT

XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

DE

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

PH 323..7108

FT /*tag= a

FT /product= "defective ABC1 polypeptide"

XX

PN WO200078972-A2.

XX

XX 28-DEC-2000.

PD

XX 16-JUN-2000; 2000WO-US16765.

PF

XX 18-JUN-1999; 99US-0140264.

PR

XX 14-SEP-1999; 99US-0153872.

PR

XX 19-NOV-1999; 99US-0166573.

PR

XX (CVTH-) CV THERAPEUTICS INC.

XX

PA Lawn RM, Wade D, Garvin M;

PI WPI; 2001-137812/14.

XX

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,

DR useful for the development of agents for the treatment of heart disease

PT and other disorders associated with hypercholesterolemia and

PT atherosclerosis -

XX

PS Disclosure; Page 148-154; 215pp; English.

XX

XX The present sequence encodes a human adenosine triphosphate (ATP)

CC binding cassette protein (ABC) 1 polypeptide, and is isolated from

CC a Tangier disease patient. ABC1 resides in cell membranes and utilises

CC ATP hydrolysis to transport a wide variety of substrates across the

CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated

CC mobilisation of intracellular cholesterol stores. ABC1 is defective in

CC Tangier disease, a genetic disorder characterised by abnormal

CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome

CC 9q22-9q31. The ABC1 genes and proteins are useful for developing

CC pharmaceutical agents for the treatment of heart disease and other

CC disorders associated with hypercholesterolemia and atherosclerosis. The

CC genes are useful for developing screening assays to screen for compounds

CC that regulate the expression of genes associated with cholesterol

CC transport. The genes and proteins are also useful for are also useful

CC as diagnostic indicators of cardiovascular disease and other disorders

CC associated with hypercholesterolemia.

XX

XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

SQ

Query Match 99.5%; Score 773; DB 22; Length 10474;

Best Local Similarity 100.0%; Pred. No. 1e-164;

Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60

|||||

Db 9532 GTAAACCTAATTTGTGGTAGAAATTTTACCACCTCTATCTCAATCAAGCAAAATTTCTG 9591

QY 61 TATATTCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATAGCTGTTCAAA 120

|||||

Db 9592 TATATTCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATAGCTGTTCAAA 9651

QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTTATTACAACACTGTGAATATGA 180

|||||

Db 9652 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTTATTACAACACTGTGAATATGA 9711

QY 181 GAAATACAGAGAAAATAATTAAGCCCTCTATACATAAATGCCACACAAATTCATTTGTTA 240

|||||

Db 9712 GAAATACAGAGAAAATAATTAAGCCCTCTATACATAAATGCCACACAAATTCATTTGTTA 9771

QY 241 AAAACACACAAACCTCACACTACTGTATTTCTATCTGTTACTGTAAGCAAAATAGCTTTG 300

|||||

Db 9772 AAAACACACAAACCTCACACTACTGTATTTCTATCTGTTACTGTAAGCAAAATAGCTTTG 9831

QY 301 TGACTATTAAATGTTTGCACATCATTCATCTCACTGTATAGTAAATTCAGTAAAGCCATT 360

|||||

Db 9832 TGACTATTAAATGTTTGCACATCATTCATCTCACTGTATAGTAAATTCAGTAAAGCCATT 9891

QY 361 TGCTGTGTTTCTTCTTGTGNTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGT 420

|||||

Db 9892 TGCTGTGTTTCTTCTTGTGNTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGT 9951

QY 421 GTCATGTATATCTGAACCTTTTGATATTGAGACATTAAATTTGGACCTTGGTATTATCTA 480

|||||

Db 9952 GTCATGTATATCTGAACCTTTTGATATTGAGACATTAAATTTGGACCTTGGTATTATCTA 10011

QY 481 CTAGAATATGTAACTACTGNAGAAATATTCCTCAATCTTTTCAAAATGGTGCATCCGCC 540

|||||

Db 10012 CTAGAATATGTAACTACTGNAGAAATATTCCTCAATCTTTTCAAAATGGTGCATCCGCC 10071

QY 541 TTAAAANGTTCATTTCCATAAGGATTTAGCTTGCTTATCCCTCTTATACCTAAGATG 500

|||||

Db 10072 TTAAAANGTTCATTTCCATAAGGATTTAGCTTGCTTATCCCTCTTATACCTAAGATG 10131

QY 601 AAGCTGTTTTTGTGCTCTTTTGTTCATCATTCATGGCCCTCATTCCTCAAGCACTTTACGCTGTCT 660

|||||

Db 10132 AAGCTGTTTTTGTGCTCTTTTGTTCATCATTCATGGCCCTCATTCCTCAAGCACTTTACGCTGTCT 10191

QY 661 GTAATGGGATCTATTTTGCACCTGGAATATCTGAGAATTCGAAAACCTAGACAAAATGTTTC 720

|||||

Db 10192 GTAATGGGATCTATTTTGCACCTGGAATATCTGAGAATTCGAAAACCTAGACAAAATGTTTC 10251

QY 721 ACAACAGATTCTTAAAGTAAATCAATTTTCATTAAGGAGAAAGAAAAAATTTT 777

|||||

Db 10252 ACAACAGATTCTTAAAGTAAATCAATTTTCATTAAGGAGAAAGAAAAAATTTT 10308

RESULT 6

AAF24686

ID AAF24686 standard; DNA; 10474 BP.

XX AAF24686;

AC AAF24686;

XX

XX 20-APR-2001 (first entry)

DT

XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

DE

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

PH 323..7108

FT /*tag= a

FT /product= "defective ABC1 polypeptide"

XX

CC The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

XX
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 1e-164;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 9532 GTAACCTAATGTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 9591
QY 61 TATATCCCTGTGAAGTACCTATGAGTTTCAGAAATCTCAAAATACGTTTCAAA 120
DB 9592 TATATCCCTGTGAAGTACCTATGAGTTTCAGAAATCTCAAAATACGTTTCAAA 9651
QY 121 AATTCTGCTTTTGGACACCTCAGAAACTTATTAAACACTGTGAATATGA 180
DB 9652 AATTCTGCTTTTGGACACCTCAGAAACTTATTAAACACTGTGAATATGA 9711
QY 181 GAATACAGAGAAATAAATAGCCCTCTATACATAATGCCAGCAATTCATTTGTA 240
DB 9712 GAATACAGAGAAATAAATAGCCCTCTATACATAATGCCAGCAATTCATTTGTA 9771
QY 241 AAAAACAACCAAACTCAGACTACTGTATTTTCAATTTCTGTTGAAAGCAAAATGCTTTG 300
DB 9772 AAAAACAACCAAACTCAGACTACTGTATTTTCAATTTCTGTTGAAAGCAAAATGCTTTG 9831
QY 301 TGACTATAATGTGACATCAATTCATCTGATAGTAATCAATTTGACATAAGCCATT 360
DB 9832 TGACTATAATGTGACATCAATTCATCTGATAGTAATCAATTTGACATAAGCCATT 9891
QY 361 TGCTGTGTTTCTTGTGGTGNATATATCAGTTAAATATTTTCCAAAGAGCCATGT 420
DB 9892 TGCTGTGTTTCTTGTGGTGNATATATCAGTTAAATATTTTCCAAAGAGCCATGT 9951
QY 421 GTCATGTAATGTAACCCCTTTGATATGAGACATTAATTTGGACCTTTGGTATATCTA 480
DB 9952 GTCATGTAATGTAACCCCTTTGATATGAGACATTAATTTGGACCTTTGGTATATCTA 10011
QY 481 CTAGAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 540
DB 10012 CTAGAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 10071
QY 541 TTAAGATGTTTATTCATAGGATTTAGTCTTATCCCTTCTTATACCTCAAGATG 600
DB 10072 TTAAGATGTTTATTCATAGGATTTAGTCTTATCCCTTCTTATACCTCAAGATG 10131
QY 601 AAGCTGTTTGTGCTCTTTGTCATCATGCGCCCTCATCCAGACACTTTACGCTGTCT 660
DB 10132 AAGCTGTTTGTGCTCTTTGTCATCATGCGCCCTCATCCAGACACTTTACGCTGTCT 10191
QY 661 GTAATGGATCTATTTTGTGCTGGAATATCTGAGATTTGCAAACTAGACAAAAGTTTC 720
DB 10192 GTAATGGATCTATTTTGTGCTGGAATATCTGAGATTTGCAAACTAGACAAAAGTTTC 10251
QY 721 ACAACAGATTTCTAAGTTAAATCAATTTTCATTAAGAGAAAAGAAAAAATTTT 777

Db 10252 ACAACAGATTTCTAAGTTAAATCAATTTTCATTAAGAGAAAAGAAAAAATTTT 10308

RESULT 8
AAF24708

ID AAF24708 standard; DNA; 10474 BP.

XX
AC AAF24708;

XX
DT 20-APR-2001 (first entry)

XX
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

XX
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

XX
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

XX
KW atherosclerosis; cholesterol transport; ss.

XX
OS Homo sapiens.

XX
EH Key Location/Qualifiers

XX
FT CDS 323..7108

XX
FT /*tag= a

XX
FT /product= "defective ABC1 polypeptide"

XX
PN WO200078971-A2.

XX
PD 28-DEC-2000.

XX
PF 16-JUN-2000; 2000WO-US16591.

XX
PR 18-JUN-1999; 99US-0140264.

XX
PR 14-SEP-1999; 99US-0153872.

XX
PR 19-NOV-1999; 99US-0166573.

XX
CVTH- CV THERAPEUTICS INC.

XX
UNIW UNIV WASHINGTON.

PI Lawn RM, Wade D, Oram JF, Garvin M;

XX
WPI; 2001-137811/14.

XX
P-PSDB; AAB31367.

XX
Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis -

XX
Claim 30; Page 165-172; 21pp; English.

XX
The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

XX
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 1e-164;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 9532 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 9591
 QY 61 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 120
 Db 9592 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 9651
 QY 121 AATTCTGCTTTTCATCTTTGGACACCTCAGAAACTTATTAAACACCTGTGAATGA 180
 Db 9652 AATTCTGCTTTTCATCTTTGGACACCTCAGAAACTTATTAAACACCTGTGAATGA 9711
 QY 181 GAAATACAGAGAAATAAAGCCCTCTATACATAATGCCAGACAAATTCATTTGTTA 240
 Db 9712 GAAATACAGAGAAATAAAGCCCTCTATACATAATGCCAGACAAATTCATTTGTTA 9771
 QY 241 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 300
 Db 9772 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 9831
 QY 301 TGACTATTAATGTGACATCAATTCACCTGTATAGTAATCAATGACTAAAGCCATT 360
 Db 9832 TGACTATTAATGTGACATCAATTCACCTGTATAGTAATCAATGACTAAAGCCATT 9891
 QY 361 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 9892 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9951
 QY 421 GTCAATGAATCACTGAACCTTTTGATTTGAGACATTAATTTGACCTTGGTATTCTA 480
 Db 9952 GTCAATGAATCACTGAACCTTTTGATTTGAGACATTAATTTGACCTTGGTATTCTA 10011
 QY 481 CTAGATTAATGTAACTAGAGAAATATGCTCTAATTTCTTTCAAAATGCTGATCCCC 540
 Db 10012 CTAGATTAATGTAACTAGAGAAATATGCTCTAATTTCTTTCAAAATGCTGATCCCC 10071
 QY 541 TTAAGAGTTCTATTTCCATTAAGATTTAGCTGCTTATCCCTCTTATACCTTAAGAG 600
 Db 10072 TTAAGAGTTCTATTTCCATTAAGATTTAGCTGCTTATCCCTCTTATACCTTAAGAG 10131
 QY 601 AAGCTGTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 10132 AAGCTGTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10191
 QY 661 GATATGGATCTATTTTGCACCTGGATATCTGAGAAATGCAAACTAGACAAAAGTTTC 720
 Db 10192 GATATGGATCTATTTTGCACCTGGATATCTGAGAAATGCAAACTAGACAAAAGTTTC 10251
 QY 721 ACAACAGATTCTTAAGTTAAATCATTTTCATTAAGAGGAAAAAGAAAAATTTT 777
 Db 10252 ACAACAGATTCTTAAGTTAAATCATTTTCATTAAGAGGAAAAAGAAAAATTTT 10308

RESULT 9
 ID AAF92831
 XX AAF92831 standard; DNA; 183999 BP.
 XX AAF92831;
 XX
 DT 17-MAY-2001 (first entry)
 XX Human ABC1 genomic DNA.
 DE High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
 KW Homo sapiens.
 XX
 PN NC0200115676-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 01-SEP-2000; 2000HO-1B01492.
 XX

PR 01-SEP-1999; 9905-0151977.
 PR 15-MAR-2000; 2000US-0526193.
 XX 23-JUN-2000; 2000US-0213958.
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON GENETICS INC.
 XX
 PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
 XX WPI: 2001-244356/25.
 XX
 PT Treating a lower than normal high density lipoprotein-cholesterol
 PT (HDL-C) level, a higher than normal triglyceride level, or a
 PT cardiovascular disease, by administering a compound that modulates LXR-
 PT or RXR-mediated transcriptional activity.
 XX
 PS Claim 8; Fig 1; 317pp; English.
 XX
 CC The present invention relates to a method for treating a patient
 CC diagnosed as having a lower than normal high density
 CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
 CC triglyceride level, or a cardiovascular disease, involving
 CC administering a compound that modulates LXR- or RXR-mediated
 CC transcriptional activity or ABC1 expression or activity.
 CC The LXR gene product may be used in an assay to identify
 CC compounds useful for the treatment of a disease or condition selected a
 CC lower than normal HDL cholesterol level, a higher than normal
 CC triglyceride level, and a cardiovascular disease.
 XX

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
 Query Match 86.6%; Score 673; DB 22; Length 183999;
 Best Local Similarity 95.7%; Pred. No. 5.8e-142;
 Matches 753; Conservative 10; Mismatches 14; Indels 10; Gaps 7;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 175214 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 175273
 QY 61 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 120
 Db 175274 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 175333
 QY 121 AATTCTGCTTTTCATCTTTGGACACCTCAGAAACTTATTAAACACCTGTGAATGA 180
 Db 175334 AATTCTGCTTTTCATCTTTGGACACCTCAGAAACTTATTAAACACCTGTGAATGA 175393
 QY 181 GAAATACAGAGAAATAAAGCCCTCTATACATAATGCCAGACAAATTCATTTGTTA 240
 Db 175394 GAAATACAGAGAAATAAAGCCCTCTATACATAATGCCAGACAAATTCATTTGTTA 175453
 QY 241 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 300
 Db 175454 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 175513
 QY 301 TGACTATTAATGTGACATCAATTCACCTGTATAGTAATCAATGACTAAAGCCATT 360
 Db 175514 TGACTATTAATGTGACATCAATTCACCTGTATAGTAATCAATGACTAAAGCCATT 175573
 QY 361 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
 Db 175574 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175633
 QY 420 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
 Db 175634 TGCTGTGTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175693
 QY 479 TACTAG-AATAATGTAACTAGNAGAAATATTTGCTCTAATTTCTTT--CAAAATGGTGCAT 535
 Db 175694 TACTAGTAAATGTAACTAGNAGAAATATTTGCTCTAATTTCTTT--CAAAATGGTGCAT 175753
 QY 536 CCCCCCTTAAAG--TTCATTTCCATTAAGATTTAGCT--TGCTTATCCCTTCTTATAC 591
 Db 175753 CCCCCCTTAAAG--TTCATTTCCATTAAGATTTAGCT--TGCTTATCCCTTCTTATAC 175811

Db 175754 CCCCTTAGATGTTTCTATTTCCATGAAGATTTAGGTATGCTATTATCCCTCTTTATAC 175813
Qy 592 CCTAAGATGAAGCTGTTTTGTTGCTTTGTTGCTATTCATCATTTGGCCCTCATTCACAGCACTTT 651
Db 175814 CCTAAGATGAAGCTGTTTGTGCTGTTTGTTCATCATTTGGCCCTCATTCACAGCACTTT 175873
Qy 652 ACGCTGCTCTGAATGAGATCTATTTTGCACCTGGAATATCTGAG-AAATTCGAAAACCTAGA 710
Db 175874 ACGCTGCTCTGAATGAGATCTATTTTGCACCTGGAATATCTGAGAAATTCGAAAACCTAGA 175933
Qy 711 CAAAAGTTTCCACACAGATTTCTAAGTTAAATCAATTTTTCATTAAGAGAAAAGAAAAA 770
Db 175934 CAAAAGTTTCCACACAGATTTCTAAGTTAAATCAATTTTTCATTAAGAGAAAAGAAAAA 175993
Qy 771 AAATTTT 777
Db 175994 AAATTTT 176000
RESULT 10
AAS04049
ID AAS04049 standard; DNA; 5352 BP.
XX AAS04049;
AC
XX
XX
DT 12-SEP-2001 (first entry)
DE Human ABC1 gene, partial genomic clone #15.
XX
XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Intron 1..194
FT /*tag= a
FT /*partial
FT /*note= "3', end of intron 48; this sequence is
FT specifically claimed"
FT /*number= 48
FT exon 195..3088
FT /*tag= b
FT /*number= 49
FT /*note= "This sequence is specifically claimed"
FT misc_feature 3089..5352
FT /*tag= c
FT /*note= "3', distal sequence"
XX
XX WO200130848-A2.
XX
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-EP10886.
XX
XX 26-OCT-1999; 99EP-0402668.
XX 01-MAR-2000; 2000US-0186260.
XX
XX (AVET) AVENTIS PHARMA SA.
XX
XX Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI Dean M;
XX
XX WPI; 2001-316327/33.
XX
XX New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX
XX Claim 1; Page 179-182; 368pp; English.
PS
XX The sequence represents the nucleic acid sequence of human ABC1 gene,
CC

CC partial genomic clone #15, comprising part of intron 48, exon 49,
CC and 3' distal sequence. The nucleic acid sequence, primers and probes
CC derived from the sequence, and polypeptides and vectors are useful for
CC the prevention of atherosclerosis, in a subject affected by a dysfunction
CC in the reverse transport of cholesterol. The polypeptide encoded by the
CC ABC1 gene is useful for screening for an active ingredient for the
CC prevention or treatment of a disease resulting from dysfunction in the
CC reverse transport of cholesterol. The nucleic acids and polypeptides are
CC also useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
CC cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 5352 BP; 1675 A; 928 C; 976 G; 1772 T; 1 other;

Query Match 85.7%; Score 666; DB 22; Length 5352;
Best Local Similarity 96.8%; Pred. No. 1.2e-140;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;
QY 1 GTAAACCTAATTTGTTAGTAAATTTTACCACACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2758 GTAAACCTAATTTGTTAGTAAATTTTACCACACTCTATCTCAATCAAGCAAAATTTCTG 2817
QY 61 TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTTCAAAATACGTGTTCAA 120
DB 2818 TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTTCAAAATACGTGTTCAA 2877
QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTATTAAACAACCTGTGAATATGA 180
DB 2878 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTATTAAACAACCTGTGAATATGA 2937
QY 181 GAATACAGAGAAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
DB 2938 GAAATACAGAGAAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 2997
QY 241 AAAAAACAACCAACCTCAGACACTACTGTATTTTCAATTTTCTACTGAAAGCAAAATGTTT 300
DB 2998 AAAAAACAACCAACCTCAGACACTACTGTATTTTCAATTTTCTACTGAAAGCAAAATGTTT 3057
QY 301 TGACTATTAATGTTGCACATCATTCATTCACCTGTATAGTAATTAATGACTAAAGCCATT 360
DB 3058 TGACTATTAATGTTGCACATCATTCATTCACCTGTATAGTAATTAATGACTAAAGCCATT 3117
QY 361 TG-CTGTGTTTTCTTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGGCCATG 419
DB 3118 TGCTGTGTTTTCTTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGGCCATG 3177
QY 420 TGTCATGTAATGTAACACC-CTTTGTATTTGAGACATTAATTTGGACCCCT-TGCTATTAT 477
DB 3178 TGTCATGTAATGTAACACCCTTTGTATTTGAGACATTAATTTGGACCCCTGTATTAT 3237
QY 478 CTACTAG-ATAATGTAATGTAACCTGAGAAATATTCCTCTAATTCCTT--CAAAATGGTGCA 534
DB 3238 CTACTAGTAATGTAATGTAACCTGAGAAATATTCCTCTAATTCCTT--CAAAATGGTGCA 3297
QY 535 TCCCCCTTAAAANG-TTCTATTTCCATAAGGATTTAGCT--TGCTTATCCCTCTCTATA 590
DB 3298 TCCCCCTTAAAANG-TTCTATTTCCATAAGGATTTAGCT--TGCTTATCCCTCTCTATA 3357
QY 591 CCCTAAGATGAAGCTGTTTTTGTGCTCTTTTGTTCATCATTTGGCCCTCATTCGAGCACTT 650
DB 3358 CCCTAAGATGAAGCTGTTTTTGTGCTCTTTTGTTCATCATTTGGCCCTCATTCGAGCACTT 3417
QY 651 TACGCTCTGTAATGGGATCTATTTTGCACCTGGAATATCTGAGAAATTCGAAAACCTAGA 710
DB 3418 TACGCTCTGTAATGGGATCTATTTTGCACCTGGAATATCTGAGAAATTCGAAAACCTAGA 3477
QY 711 CAAAAGTTTCCACACAGA-TTTCCTAAGTTAAATCAATTTTCAATTAAGAGAAAAGAAAA 769
DB 3478 CAAAAGTTTCCACACAGATTTTCTAAGTTAAATCAATTTTCAATTAAGAGAAAAGAAAA 3537
QY 770 AAATTTT 777
DB 3538 AAATTTT 3545

RESULT 11
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ID AAI93913 standard; cDNA; 5097 BP.
XX
XX
AC AAI93913;
XX
XX
DT 13-NOV-2001 (first entry)
XX
XX
DE Human stomach cancer expressed polynucleotide SEQ ID NO 140.
XX
XX
KW Human; stomach cancer; marker; screening; micro-metastasis;
KW peritoneal dissemination; ss.
XX
XX
OS Homo sapiens.
XX
XX
FN WO200109317-A1.
XX
XX
PD 08-FEB-2001.
XX
XX
PF 28-JUL-2000; 2000WO-JP05063.
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XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX
PA (HELI-) HELIX RES INST.
XX
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
PI Kodama T, Midorikawa Y;
XX
XX
DR WPI; 2001-570287/64.
DR P-PSDB; AAM94035.
XX
XX
PT New Stomach cancer-associated genes, useful as markers in blood tests
PT for screening for the early stages of the disease -
XX
XX
PS Claim 1; Page 224-226; 242pp; Japanese.
XX
XX
CC The invention relates to stomach cancer-expressed genes
CC (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The
CC genes can be used as markers in blood tests for screening for the early
CC stages of the disease. The proteins and peptides can be used as targets
CC for screening for compounds to treat the disease. They can also be used
CC for predicting micro-metastases. The gene can predict peritoneal
CC dissemination.
XX
SQ Sequence 5097 BP; 1495 A; 991 C; 1010 G; 1601 T; 0 other;
Query Match. 85.5%; Score 664.2; DB 22; Length 5097;
Best Local Similarity 96.6%; Pred. No. 2.9e-140;
Matches 741; Conservative 0; Mismatches 17; Indels 9; Gaps 6;
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DB 4331 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 4390
QY 61 TATATTCCTGTGGATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTCAA 120
DB 4391 TATATTCCTGTGGATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTCAA 4450
QY 121 AATTTCCTGTGGATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTCAA 180
DB 4451 AATTTCCTGTGGATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTGTCAA 4510
QY 181 GAAATACAGAGAAATATAATACCTCTATACATAAATGCCAGCAAAATTCATTGTTA 240
|||||

DB 4511 GAAATACAGAGAAATATAATACCTCTATACATAAATGCCAGCACAAATTCATTGTTA 4570
QY 241 AAAACAACCAACCTCACACTACTGTATTTTTCATTTCTGTACTGTAAAGCAAAATCTTTG 300
|||||
DB 4571 AAAACAACCAACCTCACACTACTGTATTTTTCATTTCTGTACTGTAAAGCAAAATCTTTG 4630
QY 301 TGAATTAATGTTGTCACATCAATTCATCTACTGTATAGTAATCAATGACTAAAGCCATT 360
|||||
DB 4631 TGAATTAATGTTGTCACATCAATTCATCTACTGTATAGTAATCAATGACTAAAGCCATT 4690
QY 361 T-GCTGTGTTTCTTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATTG 419
|||||
DB 4691 TATCTGTGTTTCTTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATTG 4750
QY 420 TGTATGTAATGTAAGCC-CTTTGATATGAGACATTAATTTGGACCTTGGTATTATC 478
|||||
DB 4751 TGTATGTAATGTAAGCC-CTTTGATATGAGACATTAATTTGGACCTTGGTATTATC 4810
QY 479 TACTAG-AATAATGTAATGTAAGCC-CTTTGATATGAGACATTAATTTGGACCTTGGTATTATC 535
|||||
DB 4811 TACTAGTAATGTAAGCC-CTTTGATATGAGACATTAATTTGGACCTTGGTATTATC 4870
QY 536 CCCCCTTAAAG-CTTCTATTTCCATAGGATTTAGCT---TGCTTATCCCTTCTTATAC 591
|||||
DB 4871 CCCCCTTAAAG-CTTCTATTTCCATAGGATTTAGCT---TGCTTATCCCTTCTTATAC 4930
QY 592 CTTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGCCCTCATTTCCAAGCACTTT 651
|||||
DB 4931 CTTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGCCCTCATTTCCAAGCACTTT 4990
QY 652 AGCTGCTCTGTAATGGGATCTATTTTGCACCTGGATATCTCAGAAATGCAAAAGTACAG 711
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DB 4991 AGCTGCTCTGTAATGGGATCTATTTTGCACCTGGATATCTCAGAAATGCAAAAGTACAG 5050
QY 712 AAAAGTTTCAACACAGATTTCTAAGTTAAATCAATTTTCAATTTTCAAAAGG 758
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DB 5051 AAAAGTTTCAACACAGATTTCTAAGTTAAATCAATTTTCAATTTTCAAAAGG 5097

RESULT 12
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ID AAH18233 standard; cDNA; 5097 BP.
XX
XX
AC AAH18233;
XX
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:18170.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602

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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	39.6	5.1	837	4	US-08-998-416-288
C 3	39.6	5.1	7218	1	US-08-332-463-14
C 4	39	5.0	6265	4	US-09-129-112-3
C 5	38	4.9	1349	2	US-08-676-782-10
C 6	37.8	4.9	1164	3	US-08-794-796-1
C 7	37.8	4.9	5433	3	US-08-929-329-1
C 8	37.2	4.8	6124	4	US-08-213-4198-3
C 9	36.6	4.7	1149	4	US-09-134-001C-2612
C 10	36.6	4.7	1189	1	US-08-307-591-2
C 11	36.2	4.7	1578	4	US-09-044-404A-1
C 12	36.2	4.7	2637	4	US-09-134-001C-1541
C 13	36.2	4.7	21234	4	US-09-810-671-3
C 14	35.6	4.6	1864	4	US-09-468-265-4
C 15	35.4	4.6	912	4	US-09-134-001C-1352
C 16	35.4	4.6	3095	6	5231168-1
C 17	34.8	4.5	610	1	US-08-463-115-50
C 18	34.8	4.5	610	1	US-08-465-388-50
C 19	34.8	4.5	785	4	US-08-936-165A-82
C 20	34.8	4.5	1835	4	US-09-512-342-2
C 21	34.8	4.5	2861	1	US-08-299-953-1
C 22	34.8	4.5	2861	1	US-08-459-415-1
C 23	34.8	4.5	2861	4	US-09-066-687-1
C 24	34.8	4.5	2861	5	PCT-US95-11231-1
C 25	34.8	4.5	3881	1	US-08-299-953-2
C 26	34.8	4.5	3881	1	US-08-459-415-2
C 27	34.8	4.5	3881	4	US-09-066-687-2

C 28	34.8	4.5	3881	5	PCT-US95-11231-2
C 29	34.8	4.5	4673	1	US-07-638-431-1
C 30	34.8	4.5	4673	5	PCT-US92-00018-1
C 31	34.6	4.5	789	6	5219739-8
C 32	34.6	4.5	1001	4	US-09-641-638-465
C 33	34.6	4.5	1001	4	US-09-641-638-466
C 34	34.6	4.5	1002	4	US-09-641-638-595
C 35	34.6	4.5	1101	4	US-09-134-001C-2665
C 36	34.4	4.4	1864	4	US-09-468-265-4
C 37	34.4	4.4	2875	3	US-08-714-918-8
C 38	34.4	4.4	2875	4	US-09-265-315-8
C 39	34.4	4.4	2875	4	US-09-265-315-8
C 40	34.4	4.4	2875	4	US-09-266-417-8
C 41	34.2	4.4	2360	1	US-08-039-364-1
C 42	34.2	4.4	2360	4	US-09-158-710-1
C 43	34.2	4.4	3095	6	5231168-1
C 44	34.2	4.4	19124	2	US-08-487-826B-13
C 45	34	4.4	874	3	US-09-020-033-2

ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglund Ran Olafsdottir
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345, 2001-000
; CURRENT APPLICATION NUMBER: US/09/426, 290
; NUMBER FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 168575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21181)...(21403)
; NAME/KEY: CDS
; LOCATION: (95252)...(95430)
; NAME/KEY: CDS
; LOCATION: (101753)...(101996)
; NAME/KEY: CDS
; LOCATION: (110324)...(110439)
; NAME/KEY: CDS
; LOCATION: (124058)...(124278)
; NAME/KEY: CDS
; LOCATION: (127009)...(127130)
; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
US-09-426-290-1
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Best Local Similarity 47.3%; Pred. No. 0.46;
Matches 129; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 55	TTTCTGTATATTCCTGCTGGAAATGACCTATGTCAGTTTCAGAAATTCCTCAAAATACGTG	114
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QY 115	TTCAAAATTTCTGCTTTTCATCTTTGGACACCTTCAGAAATTCCTTAACTCTGA	174
Db 14929	GTAATATTAATTAATTTTACATATTTAAAAAATCCAGTTGTATTTTAAACAGTACTGA	14870
QY 175	ATATGAAATACAGAGAAATTAATAAGCCCTCTATACATAATGCCACGACATTTCA	234
Db 14869	AAAGTAGAATTATAGGGAACTTGTATATACTTTCAGATGACATCTCCCCCAAGAGAA	14810

QY	356	CCATTGCTGCTGTTTCTTCTTGCTGGTGNATATATCATCAGGTAAATAATTTTCCAAAGAGC	415
Db	1137	YY	1196
QY	416	CANGTGCATGTAATACGAACCCCTTCATATTCGAGACATTAATTGGACCCCTTGCTATT	475
Db	1197	YY	1256
QY	476	ATCTACTAGAAATAATGTAATACCTGNAGAAATATGCTCTAAITCTTTCAAAATGGTGCAT	535
Db	1257	YY	1316
QY	536	CCCCCTTAAANGTCTATTTCCTCAAGGATTATAGCTGCTTATCCCTTCTTATACCCCTA	595
Db	1317	YY	1376
QY	596	AGATGAAGCTGTTTGTGCTCTTTGTTCATCATGCGCCATTCGAACAGCATTTACGC	655
Db	1377	YY	1436
QY	656	TGCTCTGAATGGATCTATTTTTTCGACTGGAATATCTGAGAAAT	699
Db	1437	ACCAATTTCTTCTATCTTTTAACTACTTGCATAGATAGGTAAT	1480
RESULT 4			
US-09-129-112-3/c			
; Sequence 3, Application US/09129112			
; Patent No. 6465716			
; GENERAL INFORMATION:			
; APPLICANT: Etzler, Marilyn B.			
; APPLICANT: Murphy, Judith B.			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Root			
; FILE REFERENCE: 023070-079810US			
; CURRENT APPLICATION NUMBER: US/09/129,112			
; CURRENT FILING DATE: 1998-08-04			
; PRIOR APPLICATION NUMBER: US 08/907,226			
; PRIOR FILING DATE: 1997-08-06			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 3			
; LENGTH: 6265			
; TYPE: DNA			
; ORGANISM: Dolichos biflorus			
; FEATURE:			
; OTHER INFORMATION: genomic sequence of NBP45 (DB46)			
; NAME/KEY: exon			
; LOCATION: (633)..(944)			
; NAME/KEY: intron			
; LOCATION: (945)..(1022)			
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; LOCATION: (1023)..(1151)			
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; LOCATION: (1152)..(1559)			
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; NAME/KEY: intron			
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; NAME/KEY: exon			
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Matches 129; Conservative 0; Mismatches 150; Indels 0; Gaps			
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QY	122	ATTTCGCTTTTGCATCTTTGGGACACCTCAGAAAACATTATTAACAACCTGTGAATATGAG	181

US-09-134-001C-2612/c

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RESULT 15
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: Sequence 1352, Application US/09134001C
: Patent No. 5380370
: GENERAL INFORMATION:
: APPLICANT: LYNN DOUCETTE-STAMM et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
: TITLE OF INVENTION: EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS

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; CURRENT APPLICATION NUMBER: US/09/134,001C
;
; CURRENT FILING DATE: 1998-08-13
;
; PRIOR APPLICATION NUMBER: US 60/064,964
;
; PRIOR FILING DATE: 1997-11-08
;
; PRIOR APPLICATION NUMBER: US 60/055,779
;
; PRIOR FILING DATE: 1997-08-14
;
; NUMBER OF SEQ ID NOS: 5674
;
; SEQ ID NO 1352
;
; LENGTH: 912
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; TYPE: DNA
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; ORGANISM: Staphylococcus epidermidis
;
; US-09-134-001C-1352

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(without alignments)
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Title: US-09-595-526c-1_COPY_9500_10276

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Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	338	43.5	8925	9	Sequence 1422, Ap
4	331	42.6	2894	9	US-09-802-640-27
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6	331	42.6	2894	9	US-09-984-827-85
7	331	42.6	2894	9	US-09-984-827-86
8	331	42.6	2894	9	US-09-984-827-87
9	331	42.6	2894	9	US-09-984-827-88
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11	331	42.6	9741	9	US-09-984-827-90
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16	331	42.6	9870	9	US-09-984-827-95
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ALIGNMENTS

RESULT 1

US-09-984-827-22
; Sequence 22, Application US/09984827
; Publication No. US20030056234A1

; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REQUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22

; LENGTH: 5352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (374)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-22

Query Match 85.7%; Score 666; DB 9; Length 5352;
Best Local Similarity 96.8%; Pred. No. 7.5e-145;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;

QY 1 GTAACCTAATTGTGTAGAAATTTTACCACTCTATCTCAATCAACGCAAAATTCG 60
|||||
DB 2758 GTAACCTAATTGTGTAGAAATTTTACCACTCTATCTCAATCAACGCAAAATTCG 2817
|||||
QY 61 TATATTCCCTGTGGGAATGACCTATGTAGTTTCAGAAATTCACAAATACGTTGTCAAA 120
|||||
DB 2818 TATATTCCCTGTGGGAATGACCTATGTAGTTTCAGAAATTCACAAATACGTTGTCAAA 2877
|||||

Sequence 99, Appl
Sequence 100, Appl
Sequence 101, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 105, Appl
Sequence 106, Appl
Sequence 107, Appl
Sequence 108, Appl
Sequence 109, Appl
Sequence 110, Appl
Sequence 111, Appl
Sequence 112, Appl
Sequence 113, Appl
Sequence 114, Appl
Sequence 115, Appl
Sequence 116, Appl
Sequence 117, Appl
Sequence 118, Appl
Sequence 119, Appl
Sequence 120, Appl
Sequence 121, Appl
Sequence 122, Appl
Sequence 123, Appl
Sequence 124, Appl

20 331 42.6 9870 9 US-09-984-827-99
21 331 42.6 9870 9 US-09-984-827-100
22 331 42.6 9870 9 US-09-984-827-101
23 331 42.6 9870 9 US-09-984-827-102
24 331 42.6 9870 9 US-09-984-827-103
25 331 42.6 9870 9 US-09-984-827-104
26 331 42.6 9870 9 US-09-984-827-105
27 331 42.6 9870 9 US-09-984-827-106
28 331 42.6 9870 9 US-09-984-827-107
29 331 42.6 9870 9 US-09-984-827-108
30 331 42.6 9870 9 US-09-984-827-109
31 331 42.6 9870 9 US-09-984-827-110
32 331 42.6 9870 9 US-09-984-827-111
33 331 42.6 9870 9 US-09-984-827-112
34 331 42.6 9870 9 US-09-984-827-113
35 331 42.6 9870 9 US-09-984-827-114
36 331 42.6 9870 9 US-09-984-827-115
37 331 42.6 9870 9 US-09-984-827-116
38 331 42.6 9870 9 US-09-984-827-117
39 331 42.6 9870 9 US-09-984-827-118
40 331 42.6 9870 9 US-09-984-827-119
41 331 42.6 9870 9 US-09-984-827-120
42 331 42.6 9870 9 US-09-984-827-121
43 331 42.6 9870 9 US-09-984-827-122
44 331 42.6 9870 9 US-09-984-827-123
45 331 42.6 9870 9 US-09-984-827-124

QY 121 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACTGTGAATATGA 180
 Db 2878 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACTGTGAATATGA 2937
 QY 181 GAAATCAGAGAAATAATAAGCCCTCTATACATAAATGCCAGACAAATTCATTTGTTA 240
 Db 2938 GAAATCAGAGAAATAATAAGCCCTCTATACATAAATGCCAGACAAATTCATTTGTTA 2997
 QY 241 AAAAAACCAACCAACCTCAGACTACTCTATTTCATTTCTGTACTGAAAGCAATGCTTTG 300
 Db 2998 AAAAAACCAACCAACCTCAGACTACTCTATTTCATTTCTGTACTGAAAGCAATGCTTTG 3057
 QY 301 TGACTATTAAATGTTGCACATCAATTCATTCAGTATAGTAAATGCTAAAGCCATT 360
 Db 3058 TGACTATTAAATGTTGCACATCAATTCATTCAGTATAGTAAATGCTAAAGCCATT 3117
 QY 361 TG-CTGTTTCTTCTTCTGTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 419
 Db 3118 TGCTGTTTCTTCTTCTGTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 3177
 QY 420 TGTCATGTAATCTGAACC-CTTTGATATTGAGACATTAATTTGGACCCCT-TGGTATTAT 477
 Db 3178 TGTCATGTAATCTGAACCCTTTGATATTGAGACATTAATTTGGACCCCTGTTATTAT 3237
 QY 478 CTACTAG-ATAATGTAATCTAGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCA 534
 Db 3238 CTACTAGTAATGTAATCTAGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCA 3297
 QY 535 TCCCCCTTAAANG-TTCTATTCCATAAGGATTAGCT--TGCTTATCCCTTCTTATA 590
 Db 3298 TCCCCCTTAAANG-TTCTATTCCATAAGGATTAGCT--TGCTTATCCCTTCTTATA 3357
 QY 591 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGCCCCCTCAATCCAAAGCACTT 650
 Db 3358 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGCCCCCTCAATCCAAAGCACTT 3417
 QY 651 TAGCGTCTGTAAGGGATCTATTTTGCATCGAATATCTGAGAAATGCAAACTAGA 710
 Db 3418 TAGCGTCTGTAAGGGATCTATTTTGCATCGAATATCTGAGAAATGCAAACTAGA 3477
 QY 711 CAAAGTTTCAACACAGA-TTTCTAAGTAAATCATTTTCAATTAAGGAAAGAAAAA 769
 Db 3478 CAAAGTTTCAACACAGATTTTCTAAGTAAATCATTTTCAATTAAGGAAAGAAAAA 3537
 QY 770 AAAAAATTT 777
 Db 3538 AAAAAATTT 3545

RESULT 2
 US-09-880-107-1422/c
 ; Sequence 1422, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 1422
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA521292
 US-09-880-107-1422
 Query Match 63.6%; Score 494.4; DB 10; Length 601;
 Best Local Similarity 96.0%; Pred. No. 1.9e-105;
 Matches 570; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
 QY 189 GAAGAAATATAAGCCCTCTATACATAAATGCCAGACAAATTCATTTGTTAAAAACAA 248
 Db 601 GAAGAAATATAAGCCCTCTATACATAAATGCCAGACAAATTCATTTGTTAAAAACAA 542
 QY 249 CCAACCTCAGACTACTGTTATTCATTTCTGTACTGAAAGCAATGCTTTGTCATATT 308
 Db 541 CCAACCTCAGACTACTGTTATTCATTTCTGTACTGAAAGCAATGCTTTGTCATATT 482
 QY 309 AAATGTTGCACATCAATTCATTCAGTATAGTAAATGCTAAAGCCATTG-CTGTG 367
 Db 481 AAATGTTGCACATCAATTCATTCAGTATAGTAAATGCTAAAGCCATTGCTGTG 422
 QY 368 TTTTCTTCTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATGTCATGT 427
 Db 421 TTTTCTTCTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATGTCATGT 362
 QY 428 AATCTGAACC-CTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTACTAG-A 485
 Db 361 AATCTGAACCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTACTAGTA 302
 QY 486 ATAATGTAATCTAGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCAATCCCCCTTA 543
 Db 301 ATAATGTAATCTAGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCAATCCCCCTTA 242
 QY 544 AAANG-TTCTATTCCATAAGGATTAGCT--TGCTTATCCCTTCTATACCCCTAAGAT 599
 Db 241 GAATGTTTCTATTTCCATAAGGATTAGGATAGTATGCTATTATCCCTTCTATACCCCTAAGAT 182
 QY 600 GAAGCTGTTTGTGCTCTTTGTCATCATTTGCCCCCTCAATCCAAAGCACTTTAGCGTGC 659
 Db 181 GAAGCTGTTTGTGCTCTTTGTCATCATTTGCCCCCTCAATCCAAAGCACTTTAGCGTGC 122
 QY 660 TGTAATGGATCTATTTTGCACCTGGAATATCTGAGAAATGCAAACTAGACAAAAGTTT 719
 Db 121 TGTAATGGATCTATTTTGCACCTGGAATATCTGAGAAATGCAAACTAGACAAAAGTTT 62
 QY 720 CACAACAGATTTCTAAGTAAATCATTTTCAATTAAGGAAAGAAAAA 773
 Db 61 CACAACAGATTTCTAAGTAAATCATTTTCAATTAAGGAAAGAAAAA 8

RESULT 3
 US-09-802-640-27
 ; Sequence 27, Application US/09802640
 ; Publication No. US20030036057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Braun, Andreas
 ; APPLICANT: Bonsal Aruna
 ; APPLICANT: Klyen Patrick
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
 ; FILE REFERENCE: 24736-2048
 ; CURRENT APPLICATION NUMBER: US/09/802,640
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 8925
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (5020)...(6162)
 ; OTHER INFORMATION: Nucleotide encoding ATP-binding cassette (ABC1)
 ; OTHER INFORMATION: n= a or g or c or t

US-09-802-640-27

Query Match 43.5%; Score 338; DB 9; Length 8925;
Best Local Similarity 100.0%; Pred. No. 1.2e-68;
Matches 338; Conservative 0; Mismatches 0; Indels

QY	1	GTAAACCTAATTGTGGTAGAAATTTTTCACAACTCTATACAACTCAAGCAAAATTTCTG	60
Db	8588	GTAAACCTAATTGTGGTAGAAATTTTTCACAACTCTATACAACTCAAGCAAAATTTCTG	8647
QY	61	TATATTCCCTGTGGGAATGTAACCTATGTGAGTTTCAGAAATTTCTCAAATACGTGTCAAA	120
Db	8648	TATATTCCCTGTGGGAATGTAACCTATGTGAGTTTCAGAAATTTCTCAAATACGTGTCAAA	8707
QY	121	AAATTCGTGCTTTTGGCATCTTTGGGCACCTCAGAAAACTTATTACAACTCTGAATATGA	180
Db	8708	AAATTCGTGCTTTTGGCATCTTTGGGCACCTCAGAAAACTTATTACAACTCTGAATATGA	8767
QY	181	GAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTA	240
Db	8768	GAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTA	8827
QY	241	AAAAACAACCAACCTCACACTACGTGTAATTCATTATCTGTAAGCAAGTGCCTTG	300
Db	8828	AAAAACAACCAACCTCACACTACGTGTAATTCATTATCTGTAAGCAAGTGCCTTG	8887
QY	301	TGACTATTAAATGTTGCACATCATTCATTCACGTGATA	338
Db	8888	TGACTATTAAATGTTGCACATCATTCATTCACGTGATA	8925

RESULT 4
 US-09-984-827-84
 ; Sequence 84, Application US/09984827
 ; Publication No. US20030056234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEFFE, PATRICE
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984,827
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/254,108
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: FR 00/14037
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 84
 ; LENGTH: 2894
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (180)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-84

```

Query Match      42.69; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTAACCTAATTGCTGATAGAAATTTTACCAACTCTATACTCAATCAAGCAAATTTCTG 60
      |||
      |||
      |||
Db      2564  GTAACCTAATTGCTGATAGAAATTTTACCAACTCTATACTCAATCAAGCAAATTTCTG 2623

QY      61  TATATCCCTGTGGAAATGTAAGTGTGAGTTTCAGAAATCTCAAAATACGTGTTTCAA 120
      |||
      |||
      |||
Db      2624  TATATCCCTGTGGAAATGTAAGTGTGAGTTTCAGAAATCTCAAAATACGTGTTTCAA 2683

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Qy	121	AAATTCGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTATTACAACTCTGTAATGA	180
Db	2684	AAATTCGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTATTACAACTCTGTAATGA	2743
Qy	181	GAATATCAGAAGAAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTA	240
Db	2744	GAATATCAGAAGAAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTA	2803
Qy	241	AAAAACAACCAACCTCACACTACTGTATTTTCATTATCTGTACTGAAAGCAAAATGCTTTG	300
Db	2804	AAAAACAACCAACCTCACACTACTGTATTTTCATTATCTGTACTGAAAGCAAAATGCTTTG	2863
Qy	301	TGACTATTAATGTTGCACATCAATTCATCA	331
Db	2864	TGACTATTAATGTTGCACATCAATTCATCA	2894

```

RESULT 5
US-09-984-827-85
: Sequence 85, Application US/09984827
: Publication No. US20030056234A1
: GENERAL INFORMATION:
: APPLICANT: DENEFFE, PATRICE
: APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
: APPLICANT: ARNOULD-REGUIGNE, ISABELLE
: APPLICANT: DUVERGER, NICOLAS
: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 85
: LENGTH: 2894
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (180)
: OTHER INFORMATION: a, t, c or g
US-09-984-827-85

```

Query Match	42.6%	Score 331;	DB 9;	Length 2894;
Best Local Similarity	100.0%;	Pred. No. 3.1e-67;		
Matches 331;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy	1	GTAACCTAATTTGGTAGAAATTTTATCCAACTCTATACTCAATCAAGCAAAATTTCTG	60
Db	2564	GTAACCTAATTTGGTAGAAATTTTATCCAACTCTATACTCAATCAAGCAAAATTTCTG	2623
Qy	61	TATATTCCTGTTGGATGTACCTATCTGTAGTTTCAGAAATTTCTCAAAATACGCTGTCAAA	120
Db	2624	TATATTCCTGTTGGATGTACCTATCTGTAGTTTCAGAAATTTCTCAAAATACGCTGTCAAA	2683
Qy	121	AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACTTATTACAACTCTGAATATGA	180
Db	2684	AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACTTATTACAACTCTGAATATGA	2743
Qy	181	GAATACAGAGAAGAAATAATAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA	240
Db	2744	GAATACAGAGAAGAAATAATAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA	2803
Qy	241	AAAAACAACCAACCTCACACTACTGTATTTCAATTATCTGTACTGAAAGCAAAATGCTTTG	300
Db	2804	AAAAACAACCAACCTCACACTACTGTATTTCAATTATCTGTACTGAAAGCAAAATGCTTTG	2863

QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTTGCACATCATTCATTCA 2894

RESULT 6

US-09-984-827-86
; Sequence 86, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-86

Query Match 42.6%; Score 331; DB 9; Length 2894;

Best Local Similarity 100.0%; Pred. No. 3.1e-67; Mismatches 0; Indels 0; Gaps 0;
Matches 331; Conservative 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
|||||
Db 2564 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGCGAATGACCTATGAGTTTCAGAAATTCAGAAATTCAGTTCTCAA 120
|||||
Db 2624 TATATCCCTGCGAATGACCTATGAGTTTCAGAAATTCAGAAATTCAGTTCTCAA 2683
QY 121 AATTTCTGCTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACAACCTGTAATATGA 180
|||||
Db 2684 AATTTCTGCTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACAACCTGTAATATGA 2743
QY 181 GAAATACAGAGAAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 240
|||||
Db 2744 GAAATACAGAGAAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 2803
QY 241 AAAAAACCAACCACTCAGACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
|||||
Db 2804 AAAAAACCAACCACTCAGACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTTGCACATCATTCATTCA 2894

RESULT 7

US-09-984-827-87
; Sequence 87, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-87

Query Match 42.6%; Score 331; DB 9; Length 2894;

Best Local Similarity 100.0%; Pred. No. 3.1e-67; Mismatches 0; Indels 0; Gaps 0;
Matches 331; Conservative 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
|||||
Db 2564 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGCGAATGACCTATGAGTTTCAGAAATTCAGAAATTCAGTTCTCAA 120
|||||
Db 2624 TATATCCCTGCGAATGACCTATGAGTTTCAGAAATTCAGAAATTCAGTTCTCAA 2683
QY 121 AATTTCTGCTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACAACCTGTAATATGA 180
|||||
Db 2684 AATTTCTGCTTTGGCATCTTTGGGACACCTCAGAAACTTATTAACAACCTGTAATATGA 2743
QY 181 GAAATACAGAGAAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 240
|||||
Db 2744 GAAATACAGAGAAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 2803
QY 241 AAAAAACCAACCACTCAGACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
|||||
Db 2804 AAAAAACCAACCACTCAGACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTTGCACATCATTCATTCA 2894

RESULT 8

US-09-984-827-88
; Sequence 88, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 88
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-88

Query Match
Best Local Similarity 42.6%; Score 331; DB 9; Length 2894;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623

QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 120
Db 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 2683

QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 2743

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 2803

QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863

QY 301 TGACTATTAATGTGCACATCAATTCATCA 331
Db 2864 TGACTATTAATGTGCACATCAATTCATCA 2894

RESULT 9
US-09-984-827-89
; Sequence 89, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-89

Query Match
Best Local Similarity 42.6%; Score 331; DB 9; Length 2894;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623

QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 120
Db 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 2683

QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 2743

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 2803

QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863

QY 301 TGACTATTAATGTGCACATCAATTCATCA 331
Db 2864 TGACTATTAATGTGCACATCAATTCATCA 2894

RESULT 9
US-09-984-827-89
; Sequence 89, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-89

Query Match
Best Local Similarity 42.6%; Score 331; DB 9; Length 2894;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623

QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 120
Db 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 2683

QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 2743
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QY 1 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623

QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 120
Db 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 2683

QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 2743

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 2803

QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863

QY 301 TGACTATTAATGTGCACATCAATTCATCA 331
Db 2864 TGACTATTAATGTGCACATCAATTCATCA 2894

RESULT 10
US-09-984-827-90
; Sequence 90, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-90

Query Match
Best Local Similarity 42.6%; Score 331; DB 9; Length 2894;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623

QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 120
Db 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTGTTCAA 2683

QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 2743
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QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 240
Db 2744 CAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 2803
QY 241 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 300
Db 2804 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 2863
QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
Db 2864 TGACTATTAAATGTTGCACATCATTCATTCA 2894

RESULT 11
US-09-984-827-1
; Sequence 1, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (7009)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-1

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Best Local Similarity 100.0%; Pred. No. 5,2e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 9393 GTAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9452
QY 61 TATATCCCTGGAATGTGAGTTTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAA 120
Db 9453 TATATCCCTGGAATGTGAGTTTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAA 9512
QY 121 AATTTCTGCTTTTGATCTTTGGACACCTCAGAAAACCTATTAACTGTGAATATGA 180
Db 9513 AATTTCTGCTTTTGATCTTTGGACACCTCAGAAAACCTATTAACTGTGAATATGA 9572
QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 240
Db 9573 GAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 9632
QY 241 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 300
Db 9633 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 9692
QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
Db 9693 TGACTATTAAATGTTGCACATCATTCATTCA 9723

RESULT 12
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Deneffe, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: Fojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

Query Match 42.6%; Score 331; DB 10; Length 9741;
Best Local Similarity 100.0%; Pred. No. 5.2e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 9393 GTAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9452
QY 61 TATATCCCTGGAATGTGAGTTTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAA 120
Db 9453 TATATCCCTGGAATGTGAGTTTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAA 9512
QY 121 AATTTCTGCTTTTGATCTTTGGACACCTCAGAAAACCTATTAACTGTGAATATGA 180
Db 9513 AATTTCTGCTTTTGATCTTTGGACACCTCAGAAAACCTATTAACTGTGAATATGA 9572
QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 240
Db 9573 GAAATACAGAGAAATAAATAGCCCTCTATACATAAATGCCAGACACAATTCATTGTTA 9632
QY 241 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 300
Db 9633 AAAACACCAACCAACCTCAGACTACTGATTTTCAATTCATTCTGTACTGAAGCAAAATGCTTGG 9692
QY 301 TGACTATTAAATGTTGCACATCATTCATTCA 331
Db 9693 TGACTATTAAATGTTGCACATCATTCATTCA 9723

RESULT 13
US-09-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR

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; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-92

Query Match          42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 60
Db 9522 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 9581

QY 61 TATATTCCTCGTGGAAATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 120
Db 9582 TATATTCCTCGTGGAAATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 9641

QY 121 AATTTCTGCTTTTGGCATCTTTGGACACCTCTATACATAAATGCCGACGACAAATTCATTGTA 180
Db 9642 AATTTCTGCTTTTGGCATCTTTGGACACCTCTATACATAAATGCCGACGACAAATTCATTGTA 9701

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTA 240
Db 9702 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTA 9761

QY 241 AAAAACAACCAACCTCAGACACTACTGTATTTTCAATTCATCTGTAAGCAAAATGCTTTG 300
Db 9762 AAAAACAACCAACCTCAGACACTACTGTATTTTCAATTCATCTGTAAGCAAAATGCTTTG 9821

QY 301 TGACTATTAAATGTGACATCATTCATCA 331
Db 9822 TGACTATTAAATGTGACATCATTCATCA 9852

RESULT 14
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-94

Query Match          42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 60
Db 9522 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 9581
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; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-93

Query Match          42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 60
Db 9522 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 9581

QY 61 TATATTCCTCGTGGAAATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 120
Db 9582 TATATTCCTCGTGGAAATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 9641

QY 121 AATTTCTGCTTTTGGCATCTTTGGACACCTCTATACATAAATGCCGACGACAAATTCATTGTA 180
Db 9642 AATTTCTGCTTTTGGCATCTTTGGACACCTCTATACATAAATGCCGACGACAAATTCATTGTA 9701

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTA 240
Db 9702 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTA 9761

QY 241 AAAAACAACCAACCTCAGACACTACTGTATTTTCAATTCATCTGTAAGCAAAATGCTTTG 300
Db 9762 AAAAACAACCAACCTCAGACACTACTGTATTTTCAATTCATCTGTAAGCAAAATGCTTTG 9821

QY 301 TGACTATTAAATGTGACATCATTCATCA 331
Db 9822 TGACTATTAAATGTGACATCATTCATCA 9852

RESULT 15
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-94

Query Match          42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 60
Db 9522 GTAAACCTAATTGGTGGAGAAATTTTACCAACTCTATCTACTCAATCAAGCAAAATTTCTG 9581
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QY 61 TATATCCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTCACAAATACGTGTTCAAA 120
Db 9582 TATATCCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTCACAAATACGTGTTCAAA 9641
QY 121 AATTTCTGCTTTTGGCAATCTTTGGGACACCTCAGAAAACCTTATTAACTGTGAATATGA 180
Db 9642 AATTTCTGCTTTTGGCAATCTTTGGGACACCTCAGAAAACCTTATTAACTGTGAATATGA 9701
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACACAAATTCATTGTTA 240
Db 9702 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACACAAATTCATTGTTA 9761
QY 241 AAAACAACCAACCTCAGACTACTGTTTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
Db 9762 AAAACAACCAACCTCAGACTACTGTTTTCATTATCTGTACTGAAAGCAAAATGCTTTG 9821
QY 301 TGACTATTAAATGTTGCACATCATTCA 331
Db 9822 TGACTATTAAATGTTGCACATCATTCA 9852

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Search completed: April 4, 2003, 06:44:28
Job time : 114.152 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 878.309 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_9500_10276

Perfect score: 777

Sequence: 1 gtaaacctaattgtgttaga.....gaaaaagaaaaaaatttt 777

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	502.8	64.7	648	12	BG567118
3	486.4	64.1	624	14	BM768930
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6	444.8	57.2	646	10	AW019972

7	442.8	57.0	678	12	BE971402
8	430	55.3	506	14	BM823180
c	428.4	55.1	531	14	BQ025022
c	425.4	54.7	640	14	BM978608
11	419.4	54.0	485	14	BM830709
c	411.8	53.0	709	9	AL048433
c	411.8	52.9	624	14	BQ026286
c	399.4	51.4	499	10	AW130712
c	373.8	48.1	500	12	BG573350
c	360	46.3	458	12	BE857175
c	353	45.4	557	10	AW006879
18	343.8	44.2	443	10	AW019981
c	337.8	43.5	527	9	AI628099
c	335.4	43.2	405	9	AA493786
c	334	43.0	432	9	AA669024
c	333.8	43.0	431	9	AI802228
c	331	42.6	486	9	AI707785
c	330.2	42.5	613	14	BM780759
c	327	42.1	372	9	AA748860
c	327	42.1	451	9	AA434152
c	322	41.4	542	14	N63586
c	319.4	41.1	437	9	AI359714
c	310.6	40.0	411	10	AV661400
c	296	38.1	381	10	BE222116
c	291	37.5	479	10	AW044702
c	284	36.6	353	9	AA328447
c	280.4	36.1	3065	11	AK019548
c	280	36.0	299	9	AA731742
c	277	35.6	447	9	AI356194
c	274.8	35.4	376	10	AV656040
c	274.4	35.3	438	9	AI819556
c	268.4	34.5	270	9	AA625082
c	265.2	34.1	660	10	AV702383
c	263.4	33.9	424	9	AI241822
c	261	33.6	679	10	BB305534
c	256.2	33.0	658	12	BF703659
c	251.2	32.3	546	13	BM243763
c	248	31.9	679	10	BE532770
c	246.4	31.7	320	9	AA737119

ALIGNMENTS

RESULT 1
BM769397
LOCUS
DEFINITION K-EST0052628 S14K402 Homo sapiens cdna clone S14K402-20-F12 5',
719 bp mRNA linear EST 04-MAR-2002
K-EST0052628 S14K402 Homo sapiens cdna clone S14K402-20-F12 5',
mRNA sequence.
ACCESSION BM769397
VERSION BM769397.1 GI:190999012
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 719)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: F column: 12
High quality sequence stop: 719.

FEATURES

source

Location/Qualifiers

1..719

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S14K402-20-F12"
/clone_lib="S14K402"
/cell_line="K402"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A) RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with 3n-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library." 1 others
BASE COUNT 222 a 133 c 95 g 268 t
ORIGIN

Query Match 73.4%; Score 570; DB 14; Length 719;
Best Local Similarity 96.4%; Pred. No. 5.6e-99;
Matches 645; Conservative 0; Mismatches 15; Indels 9; Gaps 6;

QY 1 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
DB 51 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 110
QY 61 TATATCCCTGTGGAATGATACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 120
DB 111 TATATCCCTGTGGAATGATACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 170
QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAATTTCTCAAAATACGTGTCAA 180
DB 171 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAATTTCTCAAAATACGTGTCAA 230
QY 181 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCAATTCATGTGA 240
DB 231 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCAATTCATGTGA 290
QY 241 AAAACCAACCAACCTCACACTACTGTATTTTCATTTCTGTACTGAAAGCAAAATGCTTTG 300
DB 291 AAAACCAACCAACCTCACACTACTGTATTTTCATTTCTGTACTGAAAGCAAAATGCTTTG 350
QY 301 TGACTATTAAATGTGACATCAATTCATCTACTGTATTAATCAATTCATTAAGCCATT 360
DB 351 TGACTATTAAATGTGACATCAATTCATCTACTGTATTAATCAATTCATTAAGCCATT 410
QY 361 TG-CGTGTTTCTTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGACCCATG 419
DB 411 TGTCTGTGTTTCTTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGACCCATG 470
QY 420 TGTCTGTATTAATGACCC-CTTTGATATTGAGACATTAATTTGAGCCCTTGTGATATC 478
DB 471 TGTCTGTATTAATGACCC-CTTTGATATTGAGACATTAATTTGAGCCCTTGTGATATC 530
QY 479 TACTAG-AATAATGTAATCTAGNAGAAATATTGCTCTAATCTTTT-CAAAATGTGAT 535
DB 531 TACTAGTAAATGTAATCTAGNAGAAATATTGCTCTAATCTTTTCAAAATGTGAT 590
QY 536 CCCCTTTAAAG-TTCTATTTCCATAGGATTTAGCT---TGCTATCCCTTCTTATAC 591
DB 591 CCCCTTTAGATGTTCTATTTCCATAGGATTTANGTATGCTATTTATCCCTTCTTATAC 650
QY 592 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCTATGCTGCTCATTTCCAAAGCACTTT 651
DB 651 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCTATGCTGCTCATTTCCAAAGCACTTT 710

QY 652 AGCGTGTCT 660
DB 711 AGCGTGTCT 719
RESULT 2
BG567118
LOCUS
DEFINITION
602589265F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723121 5',
mRNA sequence.
ACCESSION
BG567118
VERSION
BG567118.1 GI:13574771
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 648)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM582 row: b column: 18
High quality sequence stop: 639.
Location/Qualifiers
1. 648
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4723121"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATTTGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 120 c 84 g 237 t
ORIGIN
Query Match 64.7%; Score 502.8; DB 12; Length 648;
Best Local Similarity 95.9%; Pred. No. 3.5e-86;
Matches 579; Conservative 0; Mismatches 16; Indels 9; Gaps 6;

QY 1 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
DB 44 GTAAACCTAATTTGGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 103
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 120
DB 104 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 163
QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAATTTTAACTGCTGAATATGA 180
DB 164 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAATTTTAACTGCTGAATATGA 223
QY 181 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCAATTCATTTGTTA 240
DB 224 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCAATTCATTTGTTA 283
QY 241 AAAACCAACCAACCTCACACTACTGTTTCTTATCTACTGAAAGCAAAATCTTTTC 300


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|||||
284 CAAAACACCAACCTCACACTACTGATTTTCATTATCTGTACTGAAAGCAAAATGCTTTG 343
QY TGACTATTAAATGTTCCACATCATCTTCACTGATAGTATATCATTTGACTAAGCCATT 360
Db TGACTATTAAATGTTCCACATCATCTTCACTGATAGTATATCATTTGACTAAGCCATT 403
QY TG-CTGTGTTTCTTCTGTGGTGNATATATCAGGTGATAAATATTTTCCAAAGAGCCATG 419
Db TGCTGTGTTTCTTCTGTGGTGNATATATCAGGTGATAAATATTTTCCAAAGAGCCATG 463
QY TGTCATGTAATGTAAGACC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 478
Db TGTCATGTAATGTAAGACCCTTTGATATGAGACATTAATTTGTAACCCCTTGATATATC 523
QY TACTAG-AATAAGTATATCTGAGAAATATGCTCTAATCTTTT--CAAAATGGTGCAAT 535
Db TACTAGTAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 583
QY CCCCCTTAAANGT-TCTATTTCCATAAGGATTTAGCT---TGCTATCCCTTCTTTATAC 591
Db CCCCCTTAAANGT-TCTATTTCCATAAGGATTTAGCT---TGCTATCCCTTCTTTATAC 643
QY CCGT CCGT A 595
Db CCGT A 647

RESULT 3
BM768930 624 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0051975 S14K402 Homo sapiens cDNA clone S14K402-12-H07 5',
DEFINITION mRNA sequence.
ACCESSION BM768930
VERSION BM768930.1 GI:19098545
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 624)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: H column: 07
High quality sequence stop: 624.
Location/Qualifiers
1. 624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S14K402-12-H07"
/cell_line="S14K402"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pTZ19RP1; Site:1; EcoRI;
Site:2; NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of

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EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 204 a 109 c 81 g 230 t
ORIGIN

Query Match 64.1%; Score 498.4; DB 14; Length 624;
Best Local Similarity 97.2%; Pred. No. 2.5e-85;
Matches 558; Conservative 0; Mismatches 10; Indels 6; Gaps 5;

QY 1 GTAACCTAATTTGGTGAAGAAATTTTACCACTCTATCTCAATCAACGCAAAATTTCTG 60
Db GTAAACCTAATTTGGTGAAGAAATTTTACCACTCTATCTCAATCAACGCAAAATTTCTG 110
QY 61 TATATTCCTCTGGGATGATCTATGTTTCAGAAATTTCTCAAAATACGCTGTTCAA 120
Db TATATTCCTCTGGGATGATCTATGTTTCAGAAATTTCTCAAAATACGCTGTTCAA 170
QY 121 AATTTCTGTTTTGCAICTTTGGGACACCTCAGAAACTTATTACAACTGTGAATATGA 180
Db AATTTCTGTTTTGCAICTTTGGGACACCTCAGAAACTTATTACAACTGTGAATATGA 230
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
Db GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 290
QY 241 AAAAACAACCAACCTCACACTACTGTTTATTATTTCTGTTACTGAAACCAATGCTTTG 300
Db AAAAACAACCAACCTCACACTACTGTTTATTATTTCTGTTACTGAAACCAATGCTTTG 350
QY 301 TGACTATTAAATGTTGCACATCAATTCATTCACCTGTTATAGTATATCAATGACTAAGCCATT 360
Db TGACTATTAAATGTTGCACATCAATTCATTCACCTGTTATAGTATATCAATGACTAAGCCATT 410
QY 361 TG-CTGTGTTTCTTCTGTGGTGNATATATCAGGTGATAAATATTTTCCAAAGAGCCATG 419
Db TGCTGTGTTTCTTCTGTGGTGNATATATCAGGTGATAAATATTTTCCAAAGAGCCATG 470
QY 420 TGTCATGTAATGTAAGACC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 478
Db TGTCATGTAATGTAAGACCCTTTGATATGAGACATTAATTTGTCACCCCTTGATATATC 530
QY 479 TACTAG-AATAAGTATATCTGAGAAATATGCTCTAATCTTTT--CAAAATGGTGCAAT 535
Db TACTAGTAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 590
QY CCCCCTTAAANGT-TTCTATTTCCATAAGGATTT 568
Db CCCCCTTAAANGT-TTCTATTTCCATAAGGATTT 624

RESULT 4

AA521292/c

LOCUS

DEFINITION

AA521292

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA521292 601 bp mRNA linear EST 20-AUG-1997
aa79e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827168 3',
mRNA sequence.

AA521292
AA521292.1 GI:2261835
EST.
human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 601)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 485.
 Location/Qualifiers

FEATURES

source
 1. .601
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:827188"
 /clone_lib="NCI_CGAP_GCBI"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTT-3', (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
 212 a 81 c 106 g 202 t

BASE COUNT

Query Match 63.6%; Score 494.4; DB 9; Length 601;
 Best Local Similarity 96.0%; Pred. No. 1.4e-84;
 Matches 570; Conservative 0; Mismatches 15; Indels 9; Gaps 6;

QY 189 GAAGAAATAATAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTAAAAACAA 248
 DB 601 GAAGAAATAATAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTAAAAACAA 542
 QY 249 CCAAGCTCACACTACTGTTATTCATCTGTTAGTGAAGCAATGCTTTGTGACTATT 308
 DB 541 CCAAGCTCACACTACTGTTATTCATCTGTTAGTGAAGCAATGCTTTGTGACTATT 482
 QY 309 AAATGTTGCACATCATTCATCTGTTAGTGAAGCAATGCTTTGTGACTATT 367
 DB 481 AAATGTTGCACATCATTCATCTGTTAGTGAAGCAATGCTTTGTGACTATT 422
 QY 368 TTTTCTCTCTGTTGTTGTTATATATAGGTTAAATATTTCCAAAGGCAATGTCATGT 427
 DB 421 TTTTCTCTCTGTTGTTGTTATATATAGGTTAAATATTTCCAAAGGCAATGTCATGT 362
 QY 428 ATACTGAACC-CTTTGATTTGACATTAATTTGGACCTTGTATTAATCTAGT-A 485
 DB 361 ATACTGAACCCTTTGATTTGACATTAATTTGGACCTTGTATTAATCTAGT-A 302
 QY 486 ATAAATGTAATAGTGAAGAAATATGCTCTAATTTCTT--CAAAATGGTGCATCCGCCCTTA 543
 DB 301 ATAAATGTAATAGTGAAGAAATATGCTCTAATTTCTT--CAAAATGGTGCATCCGCCCTTA 242
 QY 544 AAAG-TTCTATTTCCATAAGCAATTTAGCT--TGCCTTATCCCTTTATACCCCTAAGAT 599
 DB 241 GAATGTTCTATTTCCATAAGCAATTTAGCT--TGCCTTATCCCTTTATACCCCTAAGAT 182
 QY 600 GAAGCTGTTTTTGCTCTTTTGTTCATCTGTTGCTTCCATCCAGCACTTTAGCTGTC 659
 DB 181 GAAGCTGTTTTTGCTCTTTTGTTCATCTGTTGCTTCCATCCAGCACTTTAGCTGTC 122
 QY 660 TGAATGGGAATCTATTTTGCACTGGAATATCTGGAATTCGAAATTCGAAACTAGCAAAAGTTT 719

DB 121 TGTATGGGATCTATTTTGGCACTGGATATCTGAGAATTCGAAAACATAGACAAAGTTT 62
 QY 720 CACAACAGATTTCTAGTTAAATCATTTTCAATTAAGGAGAAAAAGAAAAA 773
 DB 61 CACAACAGATTTCTAGTTAAATCATTTTCAATTAAGGAGAAAAAGAAAAA 8
 RESULT 5
 BG400012
 LOCUS
 DEFINITION
 mRNA sequence.
 602442068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557761 5',
 BG400012
 VERSION
 BG400012.1 GI:13293460
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapb-rs@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LICM1262 row: h column: 18
 High quality sequence stop: 614.

FEATURES

source
 Location/Qualifiers
 1. .919
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4557761"
 /clone_lib="NIH_MGC_75"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattggcc); Site_2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGCGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."
 300 a 181 c 144 g 294 t

Query Match 57.9%; Score 449.8; DB 12; Length 919;
 Best Local Similarity 92.8%; Pred. No. 4e-76;
 Matches 526; Conservative 0; Mismatches 31; Indels 10; Gaps 5;

QY 1 GTAAACCTAATTTGGTGGAGAAATTTTACCAACTCTACTCAATCAAGCAAAATTTCTG 60
 DB 127 GTAAACCTAATTTGGTGGAGAAATTTTACCAACTCTACTCAATCAAGCAAAATTTCTG 186
 QY 61 TATATCCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTTGTC 120
 DB 187 TATATCCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTTGTC 246
 QY 121 AATTTCTGCTTTTGGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATATGA 180
 DB 247 AATTTCTGCTTTTGGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATATGA 306
 QY 181 GAAATACAGAGAAAAATAATAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 240
 DB 307 GAAATACAGAGAAAAATAATAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 366


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QY 1 GTAAACCTAATTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 51 GTAAACCTAATTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 110
QY 61 TATATTCCTCGTGGATGTACCTATGTGAGTTTCAGAAATTCAGAAATACGTTGTCAAA 120
Db 111 TATATTCCTCGTGGATGTACCTATGTGAGTTTCAGAAATTCAGAAATACGTTGTCAAA 170
QY 121 AATTTCGTCTTTTGGCACTTTGGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 180
Db 171 AATTTCGTCTTTTGGCACTTTGGGACACCTCAGAAACCTTATTAACAACCTGTGAATATGA 230
QY 181 GAAATACAGAGAAATTAATAAGCCCTCTATACATATAATGCCAGCACAAATTCATTTGTTA 240
Db 231 GAAATACAGAGAAATTAATAAGCCCTCTATACATATAATGCCAGCACAAATTCATTTGTTA 290
QY 241 AAAAACAACCAACCTCACACTACTGTATTTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 300
Db 291 AAAAACAACCAACCTCACACTACTGTATTTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 350
QY 301 TGACTATTAAATGTTGCACATCAATTCATTCACCTGTATAGTAATCAATGACTAAAGCCAT 360
Db 351 TGACTATTAAATGTTGCACATCAATTCATTCACCTGTATAGTAATCAATGACTAAAGCCAT 410
QY 361 TG-CTGTGTTTCTCTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATG 419
Db 411 TGCTGTGTTTCTCTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATG 470
QY 420 TGCTGTATATAGTAAACC-CTTTGTATATTGAGACA 454
Db 471 TGCTGTATATAGTAAACCACITTTGATTGAGACA 506
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RESULT 9
BQ025022/c
LOCUS BQ025022 531 bp mRNA linear EST 27-MAR-2002
DEFINITION UI-1-BB1p-atq-b-03-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone
UI-1-BB1p-atq-b-03-0-UI 3', mRNA sequence.
ACCESSION BQ025022
VERSION BQ025022.1 GI:19760301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-atq-b-03-0-UI"
/tissue_type="NCI_CGAP_P16"
/dev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Placenta; Vector: pT73-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_P16 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
```

```
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG_LIB=UI-1-BB1p
TAG_TISSUE=placenta human full term
TAG_SEQ=AGGA"
BASE COUNT 200 a 76 c 90 g 165 t
ORIGIN
Query Match 55.1%; Score 428.4; DB 14; Length 531;
Best Local Similarity 95.5%; Pred. No. 5.4e-72;
Matches 504; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
QY 255 CTCACACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTGTGACTATTAATGT 314
Db 531 CTCACACTACTGTAATTCATTATCTGTACTGAAAGCAAAATGCTTTGTGACTATTAATGT 472
QY 315 TGCACATCAATTCATTACCTGTATAGTAATCAATGACTAAAGCCATTTG-CTGTGTTTCT 373
Db 471 TGCACATCAATTCATTACCTGTATAGTAATCAATGACTAAAGCCATTTGCTGTGTTTCT 412
QY 374 TCTTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTCATGTAATACT 433
Db 411 TCTTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTCATGTAATACT 352
QY 434 GAACC-CTTTGTATATGAGACATTAATTTGGACCTTGTGTTATCTACTAG-AATAATG 491
Db 351 GAACCCTTTGTATATGAGACATTAATTTGTACCTTGTATATCTACTAGTAATAG 292
QY 492 TAATACTGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCATCCCTTAAAG- 548
Db 291 TAATACTGNAGAAATATGCTCTAATTCCTTTTCAAAATTTGTCATCCCTTAGAATGT 232
QY 549 TTCTATTTCCATAAGGATTTAGCT--TGCTATTCCTTCTTATACCTCAAGATGAAGCT 605
Db 231 TTCTATTTCCATAAGGATTTAGTATGCTATATTCCTTCTTATACCTCAAGATGAAGCT 172
QY 606 GTTTTGTGCTCTTTGTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCTGTAAT 665
Db 171 GTTTTGTGCTCTTTGTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCTGTAAT 112
QY 666 GGGATCTATTTTGCACCTGGAATATCTGCAATTCGAAATGCAAACTAGACAAAGTTTCACAAC 725
Db 111 GGGATCTATTTTGCACCTGGAATATCTGCAATTCGAAATGCAAACTAGACAAAGTTTCACAAC 52
QY 726 AGATTTCTAAGTTAAATCAATTTTCATTAAGGAAAAAGAAAAA 773
Db 51 AGATTTCTAAGTTAAATCAATTTTCATTAAGGAAAAAGAAAAA 4
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RESULT 10
BQ978608/c
LOCUS BQ978608 640 bp mRNA linear EST 21-MAR-2002
DEFINITION UI-CF-DU1-adq-m-13-0-UI.s1 UI-Cf-DU1 Homo sapiens cDNA clone
UI-CF-DU1-adq-m-13-0-UI 3', mRNA sequence.
ACCESSION BQ978608
VERSION BQ978608.1 GI:19598215
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 640)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
```

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)
 97044477
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul.mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation by: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1. .640
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUI-adq-m-13-0-UI"
 /clone_lib="UI-CF-DUI"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUI is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells. The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GGCTGTAGGC.
 TAG_LIB=UI-CF-DUI
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_SEQ=GGCTGTAGGC"
 239 a 92 c 98 g 211 t

BASE COUNT
ORIGIN

Query Match 54.7%; Score 425.4; DB 14; Length 640;
 Best Local Similarity 95.4%; Pred. No. 1.9e-71;
 Matches 501; Conservative 0; Mismatches 15; Indels 9; Gaps 6;

QY 262 TACTGATTTTCATTCTCTACTGAAGCAATGCTTTGTGACTATTAATTTGCACAT 321
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 Db 640 TACTGATTTTCATTCTCTACTGAAGCAATGCTTTGTGACTATTAATTTGCACAT 581
 |||||
 QY 322 CATTCATTCACGTATAGTAATCAATGACTAAAGCCATTTCGTTGTTTCTTTCTTGTG 380
 |||||
 Db 580 CATTCATTCACGTATAGTAATCAATGACTAAAGCCATTTCGTTGTTTCTTTCTTGTG 521
 |||||
 QY 381 GNTGNATATACAGTAAATATTTTCCAAAGAGCCATGTCATGATATCTGAACC-C 439
 |||||
 Db 520 GTGTATATACAGTAAATATTTTCCAAAGAGCCATGTCATGATATCTGAACCAC 461
 |||||
 QY 440 TTTGATATTGAGACATTAATTTGGACCCCTTGCTATTATCTACTAG-AATAATGTAATCT 498
 |||||
 Db 460 TTTGATATTGAGACATTAATTTGTACCCCTTGTTATATCTACTAGTAATGTAATCT 401
 |||||
 QY 499 GNAAGAAATATGCTCTAATCTTTT--CAAAATGGTGCAATCCCTTAAAGG-TTCTATT 555
 |||||
 Db 400 GTAGAATATATGCTCTAATCTTTTCAAAATGTTGTCATCCCTTAAAGG-TTCTATT 341
 |||||
 QY 556 TCCATAAGGATTTAGCT---TCCTTATCCCTTCTTATACCCCTTAAGATGAAGCTGTTTTG 612
 |||||
 Db 340 TCCATAAGGATTTAGCTATGCTATTATCCCTTCTTATACCCCTTAAGATGAAGCTGTTTTG 281

QY 613 TGCTCTTTTTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCGTGTAATGGGATCT 672
 |||||
 Db 280 TGCTCTTTTTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCGTGTAATGGGATCT 221
 |||||
 QY 673 ATTTTTCACGTGGAATATCTGAGAAATTCAGAACTAGACAAAGTTTCACACACAGATTTC 732
 |||||
 Db 220 ATTTTTCACGTGGAATATCTGAGAAATTCAGAACTAGACAAAGTTTCACACACAGATTTC 161
 |||||
 QY 733 TAAGTAAATCATTTTCATTTAAAGGAAAAAGAAAAAATTTT 777
 |||||
 Db 160 TAAGTAAATCATTTTCATTTAAAGGAAAAAGAAAAAATTTT 116
 |||||

RESULT 11

BM830709

LOCUS

DEFINITION K-EST0104451 S14K402s1 Homo sapiens cDNA clone S14K402s1-22-D02 5',
 mRNA sequence.

ACCESSION BM830709

VERSION BM830709.1 GI:19187118

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 485)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL

COMMENT Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 22 row: D column: 02

High quality sequence stop: 485.

FEATURES

source

1. .485

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S14K402s1-22-D02"

/clone_lib="S14K402s1"

/cell_line="K402"

/lab_host="Top10F"

/note="Organ: Stomach; Vector: pTZ18RPL; Site 1: EcoRI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library. After analyzing and

sequencing about 2,000 ~ 3,000 colonies in original cDNA

library, the abundant cDNAs were selected and amplified by

PCR reaction using vector region primer including T7

promotor as 5' primer and N(dT)14 as 3' primer. The PCR

products were used as template for synthesis of

biotinylated single stranded RNA by in vitro transcription

reaction. The synthesized RNA probes were hybridized with

antisense single stranded cDNAs prepared from original

library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transfection of the remaining DNA into competent cells E. coli Top10P' with electroporation method."

BASE COUNT 163 a 86 c 64 g 172 t

ORIGIN
Query Match 54.0%; Score 419.4; DB 14; Length 485;
Best Local Similarity 99.1%; Pred. No. 2.9e-70;
Matches 431; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
DB 51 GTAACCTAATGTGGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 110
QY 61 TATATTCCTGCTGGAGTACCTATGTGAGTTTCAGAAATTCACAAATACGTTGTCAAA 120
DB 111 TATATTCCTGCTGGAGTACCTATGTGAGTTTCAGAAATTCACAAATACGTTGTCAAA 170
QY 121 AATTTCTGCTTTTGGACACCTCAGAAATTTTATTAACAACCTGTGAATATGA 180
DB 171 AATTTCTGCTTTTGGACACCTCAGAAATTTTATTAACAACCTGTGAATATGA 230
QY 181 GAATACAGAGAAATTAATAGCCCTCTATACATTAATGCCAGCACATTTCTATTGTTA 240
DB 231 GAATACAGAGAAATTAATAGCCCTCTATACATTAATGCCAGCACATTTCTATTGTTA 290
QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGACTGAAAGCAAAATGCTTTG 300
DB 291 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGACTGAAAGCAAAATGCTTTG 350
QY 301 TGACTATTAATGTGACATCATTCATTCACTGTATAGTAATCAATGACTAAAGCCATT 360
DB 351 TGACTATTAATGTGACATCATTCATTCACTGTATAGTAATCAATGACTAAAGCCATT 410
QY 361 TG-CTGTGTTTTCTTCTGTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATG 419
DB 411 TGCTGTGTTTTCTTCTGTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATG 470
QY 420 TGTCATGTAATCTG 434
DB 471 TGTCATGTAATCTG 485

RESULT 12
AL048433/c 709 bp mRNA linear EST 01-MAR-2000
LOCUS
DEFINITION DKFZP586I1324_r1 586 (synonym: hute1) Homo sapiens cDNA clone
ACCESSION AL048433
VERSION AL048433.1 GI:4727573
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 709)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann S.

TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Duesterhoeft A
MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
si sequence also available.
This clone (DKFZP586I1324) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

FEATURES
source
Berlin- Charlottenburg, GERMANY; Email: clone@zpd.de.
Location/Qualifiers
1..709
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP586I1324"
/tissue_lib="586 (synonym: hute1)"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

BASE COUNT 252 a 102 c 127 g 225 t

ORIGIN
Query Match 53.0%; Score 411.8; DB 9; Length 709;
Best Local Similarity 91.0%; Pred. No. 7.3e-69;
Matches 535; Conservative 0; Mismatches 39; Indels 14; Gaps 9;

QY 204 CCTCTATACATAAATGCCAGCACAAATTCATTTGTTAAAAACAA--CCAAACCTCACAC 261
DB 707 CCTCTATACATAAATGCCAGCACAAATTCATTTGTTAAAAACCAACCCCAACCTTCACAN 648
QY 262 TACTGTATTTCATTAT-CTGTACTGAAAG-CAAAATGCTTTGTGACTATTAAATGTTGCAC 319
DB 647 TACTGTATTTCATTATCCTGCTGACTGAAAGCCAAATGCTTTGTGACTATTAAATGTTGCAC 588
QY 320 ATCAATTCATCTAGTATAGTAATCAATGACTAAAGCCAAATTTG-CTGTGTTTTCTTTCTG 378
DB 587 ATCAATTCATCTAGTATAGTAATCAATGACTAAAGCCAAATTTGCTGTGTTTTCTTTCTG 528
QY 379 TGTGTCNATATATCAGTAAATATTTTCCAAAGAGCCAAATGCT-CATGTAATACATGAAC 437
DB 527 TGTGTCNATATATCAGTAAATATTTTCCAAAGAGCCAAATGCTGCTATATATACATGACC 468
QY 438 CPTTGAATTTGAGACATTAATTTGGACCTTGGTATTAATCTACT--AGAATAATGTAAT 495
DB 467 ACTTTCATATGAGACATTAATTTGGACCTTGGTATTAATCTACTAGTAATAATGTAAT 408
QY 496 ACTGNAAGTAATTTGCTCTAAATCTTTT--CAAAATGCTGATCCCTTTAAANG-TTCT 552
DB 407 ACTGNAAGTAATTTGCTCTAAATCTTTTCAAAATTTGATCCCTTTAGATGTTCT 348
QY 553 ATTCCATAAGGATTTAGCT--TGCTTATCCCTTTTATACCTAAGATGAAGCTGTTT 609
DB 347 ATTCCATAAGGATTTAGGTATGCTATATCCCTTTATACCTAAGATGAAGCTGTTT 288
QY 610 TTGTGCTTTTGTTCATCATTTGSCCTCATTCGAACACCTTTACGCTGCTGTATGGGA 669
DB 287 TTGTGCTTTTGTTCATCATTTGSCCTCATTCGAACACCTTTACGCTGCTGTATGGGA 228
QY 670 TCTATTTTTCGACTGGAATATCTGAGAATTTGCAAACTAGACAAAAGTTTCACACAGAT 729
DB 227 TCTATTTTTCGACTGGAATATCTGAGAATTTGCAAACTAGACAAAAGTTTCACACAGAT 168
QY 730 TCTAAGTTAAATCAATTTTCATTTAAAGGAAAAAGAAAAATTTT 777
DB 167 TCTAAGTTAAATCAATTTTCATTTAAAGGAAAAAGAAAAATTTT 120

RESULT 13
BQ026286/c 624 bp mRNA linear EST 27-MAR-2002
LOCUS
DEFINITION UI-1-BB1p-akp-g-08-0-UI.s2 NCI_CGAP_P16 Homo sapiens cDNA clone
UI-1-BB1p-akp-g-08-0-UI 3', mRNA sequence.
ACCESSION BQ026286
VERSION BQ026286.1 GI:19761565
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.


```

Db 319 ACITTTGATATTGAGACATTAATTTGTACCCCTTGTATTATCTACTAGTAATAATGTAATA 260
QY 497 CTGAGAAATATGCTCTTAATCTTTT--CAAAATGGTGATGCCCTTAAANG-TTCTA 553
Db 259 CTGAGAAATATGCTCTTAATCTTTTCAAAATTTGTCATCCCTCAAGAAATGTTCTA 200
QY 554 TTCCATAAGGATTTAGCTTG--CTATCCCTTCTTATACCTTAGATAGAGCTGTTT 610
Db 199 TTCCATAAGGATTTAGGATGCTATATCCCTTCTTATACCTTAGATAGAGCTGTTT 140
QY 611 TGTCCTTTTGTTCATCATTTGGCCCTCATTCACCAAGCACATTTAGCTGTCTGTAATGGAT 670
Db 139 TGTCCTTTTGTTCATCATTTGGCCCTCATTCACCAAGCACATTTAGCTGTCTGTAATGGAT 80
QY 671 CTATTTTTCGACGGAATATCTGAGAAATTCGAAACACTAGACAAAGTTTCACACAGATT 730
Db 79 CTATTTTTCGACGGAATATCTGAGAAATTCGAAACACTAGACAAAGTTTCACACAGATT 20
QY 731 TCTAAGTTAAATCATTTTC 749
Db 19 TTTAAGTTAAATCATTTTC 1

RESULT 15
BG573350
LOCUS
DEFINITION BG573350 500 bp mRNA linear EST 10-APR-2001
mRNA sequence.
ACCESSION BG573350
VERSION BG573350.1 GI:13581003
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 500)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1585 row: g column: 06
High quality sequence stop: 500.
FEATURES
Location/Qualifiers
1..500
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4724381"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: placenta; Vector: pDMR-LIB (Clontech);
Site:1: Sfil (ggccgctggcc); Site:2: Sfil (ggccattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCAGAGCGGCGGCGGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 150 a 85 c 77 g 188 t
ORIGIN

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Query Match 48.1%; Score 373.8; DB 12; Length 500;
 Best Local Similarity 94.4%; Pred. No. 1.4e-61;

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Matches 473; Conservative 0; Mismatches 16; Indels 12; Gaps 8;
QY 278 CTGTAAGTAAAGCAATGCTTTGTGACATTAATTAATGTTGCACATCAATCAATCAATCAAT 337
Db 1 CTGTAAGTAAAGCAATGCTTTGTGACATTAATTAATGTTGCACATCAATCAATCAATCAAT 59
QY 338 AGTAATCATTTGACTAAAGCCATTG--CTGTGTTTTCTTCTTGTGTTGTTGTTGTTGTTGTT 395
Db 60 AGTAATCATTTGACTAAAGCCATTGCTGTGGTGTCTTCTTGTGTTGTTGTTGTTGTTGTTGTT 119
QY 396 TAAATATATTTTCCAAAGAGCCCATGTCATGTAATTAATTAATTAATTAATTAATTAATTAAT 454
Db 120 TAAATATATTTTCCAAAGAGCCCATGTCATGTAATTAATTAATTAATTAATTAATTAATTAAT 179
QY 455 TTAATTTGGACCCCTTGGTATTATCTACTAG-AATTAATGTAATTAATTAATTAATTAATTAAT 512
Db 180 TTAATTTGGACCCCTTGGTATTATCTACTAGTAATTAATTAATTAATTAATTAATTAATTAAT 239
QY 513 CTAAATCTTTT--CAAAATGGTGATCCCTTAAANG-TTCTATTTCCATAAGGATTTA 569
Db 240 CTAAATCTTTTCAAAATTTGTCATCCCTTAGAATGTTCTATTCCATAAGGATTTA 299
QY 570 GCT---TGCTTATCCCTTCTTATACCTTAAGATGAAGCTGTTTTTGTGCTCTTTTGTTCAT 626
Db 300 GGTATGCTATTATCCCTTCTTATACCTTAAGATGAAGCTGTTTTTGTGCTCTTTTGTTCAT 359
QY 627 CATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCTGTAAATGGGATCTATTTTGCACATGGA 686
Db 360 CATTTGGCCCTCATTTCCAAAGCACTTTACGCTGTCTGTAAATGGGATCTATTTTGCACATGGA 419
QY 687 ATATCTGAGAATTTGCAAACTAGACAAAGTTTTCACACAGATTTCTTAAGTTAAATCAAT 746
Db 420 ATATCTGAGAATTTGCAAACTAGACAAAGTTTTCACACAGATTTCTTAAGTTAAATCAAT 479
QY 747 TTCATTTAAAGGAAAAAGAA 767
Db 480 TTCATTTAAAGGAAAAAGAA 500

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Search completed: April 3, 2003, 16:37:12
 Job time : 890.309 secs

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GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13444.6 Seconds
(without alignments)
14684.987 Million cell updates/sec

Title: US-09-595-526c-1_copy_291_7074

Perfect score: 6784

Sequence: 1 atgctgttgctcagct.....agtgaagaagactatgtat 6784

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sv:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pin:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6784	100.0	10442	6	AX060713 Sequence
2	6784	100.0	10442	6	AX060892 Sequence
3	6784	100.0	10442	9	AF285167 Homo sapi
4	6782.4	100.0	10474	6	AX060719 Sequence
5	6782.4	100.0	10474	6	AX060721 Sequence
6	6782.4	100.0	10474	6	AX060898 Sequence
7	6782.4	100.0	10474	6	AX060900 Sequence
8	6776	99.9	7860	6	AX092594 Sequence
9	6759.6	99.8	6786	6	AB055982 Homo sapi
10	6768	99.8	7260	6	AX253452 Sequence
11	6764.8	99.7	9741	6	AX127830 Sequence
12	6764.8	99.7	9741	6	AX139817 Sequence
13	6764.8	99.7	9741	6	AX351038 Sequence
14	6764.8	99.7	9854	6	AX127831 Sequence
15	6764.8	99.7	9854	6	AX139818 Sequence
16	6750.8	99.5	7862	6	AX135712 Sequence
17	6708	98.9	6880	6	AX253450 Sequence
18	6708	98.9	6880	9	HSA012376
19	6708	98.9	9497	6	AX059973 Sequence
20	6708	98.9	9497	9	AF165281 Homo sapi
21	6694	98.7	9495	6	AX059978 Sequence
22	6589.2	97.1	9593	6	AX059976 Sequence
23	5581	82.3	7878	10	MMAB01
24	4345.6	64.1	7074	5	AF362377 Gallus ga
25	1931.6	28.5	7298	9	AF001945 Homo sapi
26	1931.6	28.5	7709	4	BTU90126
27	1928.8	28.4	7268	10	MMAF000149
28	1926.8	28.4	7323	9	HSAF000148
29	1918.8	28.3	7276	9	HSU88667
30	1904.4	28.1	5097	9	BD012346
31	1904.4	28.1	5097	9	AK027864
32	1904.4	28.1	5097	23	BD005026
33	1742.2	25.7	6704	9	AF328787
34	1742.2	25.7	7795	6	AX429481 Sequence
35	1735.8	25.6	6027	9	AB055390 Homo sapi
36	1735.8	25.6	6432	6	AX320364 Sequence
37	1735.8	25.6	6522	6	AX202218 Sequence
38	1735.8	25.6	6588	9	AF250238 Homo sapi
39	1735.8	25.6	6768	6	AX320362 Sequence
40	1696	25.0	6607	6	AX080493 Sequence
41	1596	25.0	6607	10	AF287141 Mus muscu
42	1531.6	22.6	5762	6	AX080462 Sequence
43	1465	21.6	5669	6	AX202220 Sequence
44	985	14.5	7305	6	AX235953 Sequence
45	985	14.5	7482	9	AF327657 Homo sapi

ALIGNMENTS

RESULT 1	AX060713	Sequence 1	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060713	Sequence 1	from Patent WO0078972.			
DEFINITION	AX060713					
ACCESSION	AX060713					
VERSION	AX060713.1	GI:12406103				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 10442)					
AUTHORS	Lawn,R.M., Wade,D. and Garvin,M.					
TITLE	Regulation with binding cassette transporter protein abcl					
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;					

Pred. No. is the number of results predicted by chance to have a

CV THERAPEUTICS, INC. (US)

Location/Qualifiers
I. .10442

source
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others

ORIGIN

Query Match 100.0%; Score 6784; DB 6; Length 10442;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6784; Conservative 0; Mismatches 0; Gaps 0;

QY	1	ATGGCTGTGGCTCAGCTGAGTGGCTGCTGTGGAAGAACCTCACTTTCAGAGAAGA	60
Db	291	ATGGCTGTGGCTCAGCTGAGTGGCTGCTGTGGAAGAACCTCACTTTCAGAGAAGA	350
QY	61	CAAACTGTACAGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC	120
Db	351	CAAACTGTACAGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC	410
QY	121	TCTGTTGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	180
Db	411	TCTGTTGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	470
QY	181	ATGCCCTCTGCAGGAACACTTCTTGGGTTTCAGGGGATTAATCTGTAATGCCAAACCC	240
Db	471	ATGCCCTCTGCAGGAACACTTCTTGGGTTTCAGGGGATTAATCTGTAATGCCAAACCC	530
QY	241	TGTTTCGGTACCGACTCCTGGGAGGCTCCGGAGTGTGGAACTTTTAACTTAACTCC	300
Db	531	TGTTTCGGTACCGACTCCTGGGAGGCTCCGGAGTGTGGAACTTTTAACTTAACTCC	590
QY	301	ATTGTGGCTCGCTGTCTCAGATGCTCGAGGCTCTCTTTATACAGCCAGAAAGACACC	360
Db	591	ATTGTGGCTCGCTGTCTCAGATGCTCGAGGCTCTCTTTATACAGCCAGAAAGACACC	650
QY	361	AGCATGAAGGACATGGCAAGTCTTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA	420
Db	651	AGCATGAAGGACATGGCAAGTCTTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA	710
QY	421	AAGTTGAAGCTTCAAGATTTCCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC	480
Db	711	AAGTTGAAGCTTCAAGATTTCCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC	770
QY	481	AACTTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCATTTCCAC	540
Db	771	AACTTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCATTTCCAC	830
QY	541	AAGGTATTTTTCGAAGGCTACCAATTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	600
Db	831	AAGGTATTTTTCGAAGGCTACCAATTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	890
QY	601	GAAGAGATGATTCAACTGGTGACCAAGAAGTTCTGAGCTTTTGGCTACCAAGAGAG	660
Db	891	GAAGAGATGATTCAACTGGTGACCAAGAAGTTCTGAGCTTTTGGCTACCAAGAGAG	950
QY	661	AAACTGGGTGACGAGAGGAGTACTTCTTCCACATGGACATCTCAAGCCATCTG	720
Db	951	AAACTGGGTGACGAGAGGAGTACTTCTTCCACATGGACATCTCAAGCCATCTG	1010
QY	721	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAGGAGTGGCTGAAGCCACAAAACA	780
Db	1011	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAGGAGTGGCTGAAGCCACAAAACA	1070
QY	781	TGCTGCTAGTCTTGGACATCTGCCCCAGGAGTGTTCACATGAGAGCTGGAGTGAC	840
Db	1071	TGCTGCTAGTCTTGGACATCTGCCCCAGGAGTGTTCACATGAGAGCTGGAGTGAC	1130
QY	841	ATGCACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCAATC	900
Db	1131	ATGCACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCAATC	1190
QY	901	TACCAGGCTGTCTCTGTTTGTCTGGGGGATCCCGAGGAGGGGGCTGAGATCAAG	960

Db	1191	TACCAGGCTGTCTCTGTTTGTCTGGGGATCCGAGGAGGGGCTGAAGATCAAG	1250
QY	961	TCTCTCAACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGCAATGGCAGCTGAG	1020
Db	1251	TCTCTCAACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGCAATGGCAGCTGAG	1310
QY	1021	GAAGATGCTGAACCTCTTATGACAACTCTAACTCCTTACTGCAATGATTGATGAAG	1080
Db	1311	GAAGATGCTGAACCTCTTATGACAACTCTAACTCCTTACTGCAATGATTGATGAAG	1370
QY	1081	AATTTGGAGTCTAGTCCCTCTTCCCGGATTAATCTGGAAGCTCTGAAGCCCTGCTGTT	1140
Db	1371	AATTTGGAGTCTAGTCCCTCTTCCCGGATTAATCTGGAAGCTCTGAAGCCCTGCTGTT	1430
QY	1141	GGAGATGCTGTATACACCTGACACTCCAGCCACAGGAGGATCATGGCTGAGGTGAAC	1200
Db	1431	GGAGATGCTGTATACACCTGACACTCCAGCCACAGGAGGATCATGGCTGAGGTGAAC	1490
QY	1201	AAGACCTTCCAGGAACTGGCTGTGTCCATGATCTGGAAGCATGTGGAGGAACCTCAGC	1260
Db	1491	AAGACCTTCCAGGAACTGGCTGTGTCCATGATCTGGAAGCATGTGGAGGAACCTCAGC	1350
QY	1261	CCCAAGATCTGGACCTTCATGGAGAAGCAAGCAAAATGGACCTTGTCCGATGCTGTTG	1320
Db	1551	CCCAAGATCTGGACCTTCATGGAGAAGCAAGCAAAATGGACCTTGTCCGATGCTGTTG	1610
QY	1321	GACAGCAGGAACTAGACCTTTTGGGAAACAGCAGTGTGGATGGCTTAGATGGACAGCC	1380
Db	1611	GACAGCAGGAACTAGACCTTTTGGGAAACAGCAGTGTGGATGGCTTAGATGGACAGCC	1670
QY	1381	CAAGACATCTGGGCTTTTGGCCCAAGCAGCAGATGTCCAGTCCCACTAATGTTCT	1440
Db	1671	CAAGACATCTGGGCTTTTGGCCCAAGCAGCAGATGTCCAGTCCCACTAATGTTCT	1730
QY	1441	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCCAGGCAATCCGAGCAATCTCGC	1500
Db	1731	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCCAGGCAATCCGAGCAATCTCGC	1790
QY	1501	TTCATGAGTGTGTCAACCTGACCAAGCTAGAACCCATAGCAAGAGTCTGGCTCATC	1560
Db	1791	TTCATGAGTGTGTCAACCTGACCAAGCTAGAACCCATAGCAAGAGTCTGGCTCATC	1850
QY	1561	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTCTGGGCTGGTATGTTGTTCACTGA	1620
Db	1851	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTCTGGGCTGGTATGTTGTTCACTGA	1910
QY	1621	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACAT	1680
Db	1911	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACAT	1970
QY	1681	GACAATGTGGAGGACAAATAAATCAAGGATGGGTACTGGGACCTGGCTCCTCGAGCT	1740
Db	1971	GACAATGTGGAGGACAAATAAATCAAGGATGGGTACTGGGACCTGGCTCCTCGAGCT	2030
QY	1741	GACCCCTTTCAGGACATGCGGTAGCTCTGGGGGGCTTCCCTTACTTGCAGGATGGTG	1800
Db	2031	GACCCCTTTCAGGACATGCGGTAGCTCTGGGGGGCTTCCCTTACTTGCAGGATGGTG	2090
QY	1801	GAGCAGCAATCATCAGGGTCTGAGGGGACCGAGGAGAAACTGTGTCTATATGCAA	1860
Db	2091	GAGCAGCAATCATCAGGGTCTGAGGGGACCGAGGAGAAACTGTGTCTATATGCAA	2150
QY	1861	CAGATGCCCTTATCCCTGTTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG	1920
Db	2151	CAGATGCCCTTATCCCTGTTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG	2210
QY	1921	CCCTCTTTCATGAGCTGGCTGATTTACTCAGTGGCTGTGATCATCAAGGCATCTGTG	1980
Db	2211	CCCTCTTTCATGAGCTGGCTGATTTACTCAGTGGCTGTGATCATCAAGGCATCTGTG	2270
QY	1981	TATGAGAAGGAGCAGGCTGAAAGACCATTCGGATCATGGGCTGGACACACATCA	2040

Db 2271 TATGAGAGGAGCAGCGCTGAAAGAGACCATGCGGATCATGGGCTGGACAAACAGCATATA 2330
Qy 2041 CTCGTGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGSCCTGTGA 2100
Db 2331 CTCGTGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGSCCTGTGA 2390
Qy 2101 GTGGTCATCCTGAAGTTAGGAACCTGCTGCCCTACAGTAGATCCAGCGTGGTGTGTC 2160
Db 2391 GTGGTCATCCTGAAGTTAGGAACCTGCTGCCCTACAGTAGATCCAGCGTGGTGTGTC 2450
Qy 2161 TTCCCTGTCGCTGTTGCTGTGTGACAACTCTGCAGTGGCTTCTGATAGACACTCTTC 2220
Db 2451 TTCCCTGTCGCTGTTGCTGTGTGACAACTCTGCAGTGGCTTCTGATAGACACTCTTC 2510
Qy 2221 TCCAGAGCCAACTGCGCAGCAGCCTGTGGGGCATCATCTACTTACAGCTGTACCTGCCC 2280
Db 2511 TCCAGAGCCAACTGCGCAGCAGCCTGTGGGGCATCATCTACTTACAGCTGTACCTGCCC 2570
Qy 2281 TAGCTCCTGTGTGTCATGCGCAGGACTAGTGGGCTTACACTCAAGATCTTCGCTAGC 2340
Db 2571 TAGCTCCTGTGTGTCATGCGCAGGACTAGTGGGCTTACACTCAAGATCTTCGCTAGC 2630
Qy 2341 CTGCTGTCTCCTGCTGCTTTGGGTTGGCTGTGAGTACTTTGGCCCTTTTGGAGGACAG 2400
Db 2631 CTGCTGTCTCCTGCTGCTTTGGGTTGGCTGTGAGTACTTTGGCCCTTTTGGAGGACAG 2690
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Db 2691 GGCATTGGAGTCAGTGGGACAACTGTTTGAGAGTCTGTGGAGGAAGATGCTTCAAT 2750
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Qy 2581 ACCAAGTCTACTGTTTGGCGAGGAAGTATGAGAGGCCACCTGGTTCCTCCACACAG 2640
Db 2871 ACCAAGTCTACTGTTTGGCGAGGAAGTATGAGAGGCCACCTGGTTCCTCCACACAG 2930
Qy 2641 AAGAGATGTCAGAAATCTCATGGAGGAGGAACCCACCTGTAAGCTGGCGCTGTCC 2700
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Qy 2701 ATTCAGAACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTCTGATGCCCTGGCA 2760
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Db 3111 ACCACCATGTCAATCTGACCGGTTGTTCCTCCCGACCTCGGGCACCGCTACATCCTG 3170
Qy 2881 GGAAGAACATTCGCTCTGATGAGCAGCATCCGCGAGAACTGGGGTCTGTCCCCAG 2940
Db 3171 GGAAGAACATTCGCTCTGATGAGCAGCATCCGCGAGAACTGGGGTCTGTCCCCAG 3230
Qy 2941 CATACCTGTCTTGTACATGCTGACTGTGGAAGAACACATCTGGTTCATGCCCCGTTG 3000
Db 3231 CATACCTGTCTTGTACATGCTGACTGTGGAAGAACACATCTGGTTCATGCCCCGTTG 3290
Qy 3001 AAAGGCTCTCTGAGAGCAGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTGGT 3060
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Qy 3181 GCTGGTGGACCTTACTCCCGAGGGAATATGGGAGCTGCTCTGAATACCGGCAA 3240
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Qy 3241 GGCCGACCATTAATCTCTACACACCATGATGAAGCGGAGCTCCTGGGAGCAGG 3300
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Qy 3301 ATTGCCATCTCTCCATGGGAAGCTGTCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3360
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Qy 3481 AGCAGTCTGTGCTGGCTGGCAGCGACCATGAGTGCACGCTGACCATCGATGTC 3540
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Qy 3721 GAGACGACCTGGAGAAATATTCCTAAGGTGGCGGAGAGAGTGGGTGGATGATGAG 3780
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Db 4371 GCCTTGTGTTCAGCTGATCGTCCACCTTTGGCAAGTACCCGAGCTGGAACCTTCAG 4430
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Db 4431 CCCTGGATGTACAAAGCAGTACATTTGTTCAGCAATGATGCTCCTGAGGACACGGGA 4490

QY 4201 ACCGTGAACCTCTTAAAGCCCTCACCAGACCCCTGGCTTCGGAGCCCGCTGTATGAA 4260
DB 4491 ACCGTGAACCTCTTAAAGCCCTCACCAGACCCCTGGCTTCGGAGCCCGCTGTATGAA 4350
QY 4261 GGAACCCCAATCCAGACACCGCCCTGCCAGGCGAGGAGAGAGTGAGGACCTATGCCCA 4320
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QY 4321 GTTCCCGAGACCATCATGAGACCTCTTCCAGAATGGGAACATGGACAATGCAAGACCCCTTCA 4380
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QY 4381 CTTGCATGCCAGTGACACGACGACAAATCAAGAAGATGGCTGTGTGTCGCCCCAGGG 4440
DB 4671 CTTGCATGCCAGTGACACGACGACAAATCAAGAAGATGGCTGTGTGTCGCCCCAGGG 4730
QY 4441 GCAGGGGGCTGCTCCTCCACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTG 4500
DB 4731 GCAGGGGGCTGCTCCTCCACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTG 4790
QY 4501 ACAGGAAGAACAATTTGGGATATCTGGTGAAGACGATATGTGCAGATCATAGCCAAAAGC 4560
DB 4791 ACAGGAAGAACAATTTGGGATATCTGGTGAAGACGATATGTGCAGATCATAGCCAAAAGC 4850
QY 4561 TTAAGAAACAAGATCTGGGTGAATGATTTAGGTATGGGGCTTTTCCCTGGGTGTCAGT 4620
DB 4851 TTAAGAAACAAGATCTGGGTGAATGATTTAGGTATGGGGCTTTTCCCTGGGTGTCAGT 4910
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DB 4911 AATACCTCAAGCACTTCTCCGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAA 4970
QY 4681 CACCTAAAGCTGCCAAGACAGTCTGCAGATCGATTTCTCAACAGCTTGGAGATTT 4740
DB 4971 CACCTAAAGCTGCCAAGACAGTCTGCAGATCGATTTCTCAACAGCTTGGAGATTT 5030
QY 4741 ATGACAGGACTGACACACCAAGAAATATGTCAGGTGGTTCATTAACAAGGGCTGGCAT 4800
DB 5031 ATGACAGGACTGACACACCAAGAAATATGTCAGGTGGTTCATTAACAAGGGCTGGCAT 5090
QY 4801 GCATCAGCTCTTCTGATGATCATCAACATGCCATTCCTCGGGCCCAACCTGCAAAAG 4860
DB 5091 GCATCAGCTCTTCTGATGATCATCAACATGCCATTCCTCGGGCCCAACCTGCAAAAG 5150
QY 4861 GGAGAAACCCCTAGCCATTATGGAATTAATGCTTTCAATCATCCCTGAATCTCACCAAG 4920
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DB 5211 CAGCAGCTCTCAGAGGTGGCTCTGATGACCAATCAGTGGATGCTTGTGTCATCTGT 5270
QY 4981 GTCATCTTTGCAATGTCCTTCTCCAGCCAGCTTTGCTGATTCCTGATCCAGAGCGG 5040
DB 5271 GTCATCTTTGCAATGTCCTTCTCCAGCCAGCTTTGCTGATTCCTGATCCAGAGCGG 5330
QY 5041 GTCAGAAAGCAAAACACCTGCAAGTTCATCAGTGGAGTGAAGCCCTGTCATCTGCTC 5100
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QY 5101 TCTAATTTTGTCTGGATATGCAATACAGTTCGCTGATTCCTGATCCAGACTGGTATATCATC 5160
DB 5391 TCTAATTTTGTCTGGATATGCAATACAGTTCGCTGATTCCTGATCCAGACTGGTATATCATC 5450
QY 5161 TTCATCTGCTTCCAGCAAGTTCATGTCCTCCCAACCAATCTGCCCTGTGCTAGCCCTT 5220
DB 5451 TTCATCTGCTTCCAGCAAGTTCATGTCCTCCCAACCAATCTGCCCTGTGCTAGCCCTT 5510
QY 5221 CTACTTTTGTGTTGGTGTCAATCAGCTCTCATGTACCCAGCTCTCTTTGTGTTTC 5280
DB 5511 CTACTTTTGTGTTGGTGTCAATCAGCTCTCATGTACCCAGCTCTCTTTGTGTTTC 5570
QY 5281 AAGATCCCCAGCACAGCCTATGTGGTGTCTACCCAGCTGAACCTCTTCAATGGCATTAAT 5340

DB 5571 AAGATCCCCAGCACAGCCTATGTGGTGTCTACACGCTGAACCTCTTCAATGGCATTAAT 5630
QY 5341 GGAGCGTGGCCACCTTTGTGCTGGAGCTGTTTCAACGCAATTAAGCTGAATAATATCAAT 5400
DB 5631 GGAGCGTGGCCACCTTTGTGCTGGAGCTGTTTCAACGCAATTAAGCTGAATAATATCAAT 5690
QY 5401 GATATCCCTGAAGCTCGTGTCTTGTATCTTCCACATTTTTCCTGGGAGGAGGCTCATC 5460
DB 5691 GATATCCCTGAAGCTCGTGTCTTGTATCTTCCACATTTTTCCTGGGAGGAGGCTCATC 5750
QY 5461 GACATGGTGAAGAAACACGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT 5520
DB 5751 GACATGGTGAAGAAACACGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT 5810
QY 5521 GTGTCAACCATATCTTGGGACTTGTGGAGCAAAACCTCTTTCGCCATGGCCGTGAAGGG 5580
DB 5811 GTGTCAACCATATCTTGGGACTTGTGGAGCAAAACCTCTTTCGCCATGGCCGTGAAGGG 5870
QY 5581 GTGGTGTCTTCTCATTACTTGTCTGATCCAGTACAGATTTCTTCAATCAGCCAGACCT 5640
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ACCESSION AX060892
VERSION AX060892.1 GI:12406270
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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JOURNAL CV THERAPEUTICS, INC. (US)
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RESULT 3

AF285167

LOCUS

DEFINITION

AF285167

AF285167

AF285167.1

GI:9755158

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

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 1 (bases 1 to 10442)
 Schwartz, K., Lawn, R.M. and Wade, D.P.
 ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
 regulated by LXR
 Unpublished
 2 (bases 1 to 10442)
 Lawn, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
 Porter, J.G., Seilhamer, J.J., Vaughan, A.M. and Oram, J.F.
 Direct Submission
 Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
 3172 Porter Drive, Palo Alto, CA 94304, USA
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VERSION AX060719.1 GI:12406108
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7/28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Db	2303	TATGAGAAGGAGCAGCGCTGAAAGAGACCATGCGGATCATGGCCCTGGACAACAGCATA	2362
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Db	2363	CTCTGGTTTACGTGGTTCAATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCCTGCTA	2422
QY	2101	GTGTCATCTCTGAAGTTAGGAACCTGCTGCCCTACACTGATCCACAGCGTGGTGTGTC	2160
Db	2423	GTGTCATCTCTGAAGTTAGGAACCTGCTGCCCTACACTGATCCACAGCGTGGTGTGTC	2482
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Db	2483	TTCTGTCCGTGTTTGTGTGTGTGACAAATCCCTGTGAGTGGTTCCTGTATTAGCACACTCTTC	2542
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QY	2281	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTACACTCAAGATCTTCGTAGC	2340
Db	2603	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTACACTCAAGATCTTCGTAGC	2662

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QY	2401	GGCATTGGAGTCAGTGGGACAAACCTGTTTCAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2460
DB	2723	GGCATTGGAGTCAGTGGGACAAACCTGTTTCAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2782
QY	2461	CTCACCACATTGATCTCCATGATGCTGTTTGACACCTTCCCTCTATGGGTGATGACCTGG	2520
DB	2783	CTCACCACATTGATCTCCATGATGCTGTTTGACACCTTCCCTCTATGGGTGATGACCTGG	2842
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DB	2963	AAGAGAAATGTCAGAAATCTGATGTGAGGAGGAGAACCCACCCTTGAAGCTTGGGCGTGTCC	3022
QY	2701	ATTACAGAACCTCGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCTGGCA	2760
DB	3023	ATTACAGAACCTCGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCTGGCA	3082
QY	2761	CTGAATTTTATGAGGGCCAGATCACTCTCTTCCTGGGCCACATGAGAGCGGGGAGAGCG	2820
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QY	2821	ACCACCATGTCAATCTGTACCGGGTTGTCCCCCGAGCTCGGGCAGCGCTACATCCTG	2880
DB	3143	ACCACCATGTCAATCTGTACCGGGTTGTCCCCCGAGCTCGGGCAGCGCTACATCCTG	3202
QY	2881	GGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG	2940
DB	3203	GGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG	3262
QY	2941	CATTAACGTGCTGTTTGACATGCTGACTGTCSGAGACACATCTGTTCTATGCCCCGTG	3000
DB	3263	CATTAACGTGCTGTTTGACATGCTGACTGTCSGAGACACATCTGTTCTATGCCCCGTG	3322
QY	3001	AAAGGGCTCTCTGAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3060
DB	3323	AAAGGGCTCTCTGAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3382
QY	3061	TTGCCATCAAGCAGCTGAAAACCAAAACAGCCAGCTGTGAGTGGGAATCSGAGAAAG	3120
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 VERSION AX060721.1 GI:12406109
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 10474)
 AUTHORS Law, R.M., Wade, D. and Garvin, M.
 TITLE Regulation with binding cassette transporter protein abcl
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 10474)
 AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
 TITLE Atp binding cassette transporter protein abci polypeptides
 JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
 CV THERAPEUTICS, INC. (US)
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
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CV THERAPEUTICS, INC. (US)
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 1
 Tanaka, A.R., Abe-Dohmae, S., Arakawa, R., Sadanami, K., Kidera, A.,

Kioka, N., Anachi, T., Yokoyama, S., and Ueda, K.
 A new topological model of functional human ABCAL-signal peptide
 cleavage and glycosylation of a large extracellular domain
 Unpublished

2 (bases 1 to 6786)
 Ueda, K., Kioka, N. and Tanaka, A.R.
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 Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate

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 606-8502; Japan (E-mail: uedak@kais.kyoto-u.ac.jp,
 tel: 81-75-753-6105, fax: 81-75-753-6104)
 Location/Qualifiers

FEATURES


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D	b	3541	TCCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGCTGGTGAAGACATA	3600
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D	b	3661	CTCTTTTCATGAGATTGATCACCGGCTCTCAGACCTTGGCATTTCTAGTTATGGCATCTCA	3720
Q	y	3721	GAGACAGCCTTGAAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3780
D	b	3721	GAGACAGCCTTGAAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3780
Q	y	3781	ACCTCAGATGGTACCTTGCACAGACAGAAACAGCGGGCTTCGGGGGACAAGCAGAGC	3840
D	b	3781	ACCTCAGATGGTACCTTGCACAGACAGAAACAGCGGGCTTCGGGGGACAAGCAGAGC	3840
Q	y	3841	TGCTTTGCGCCGTTTCACTGAAGATGATGCTGTGATCCAAATGATCTTGACATAGACCCA	3900
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Q	y	3901	GAATCAGAGACAGACACTTGTCTAGTGGATGATGCCAAGAGTCTTACCAGGTGAAA	3960
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Q	y	4021	AGACGGAGTCGGAAGAGATTTTTCCTCAGATTGCTTGCACAGTGTCTGCTGCTGCATT	4080
D	b	4021	AGACGGAGTCGGAAGAGATTTTTCCTCAGATTGCTTGCACAGTGTCTGCTGCTGCATT	4080
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D	b	4081	GCCTTGTTGTTACAGCTTGATGCTGCCACCTTTGGCAAGTACCCACAGCTGGAACCTTCAG	4140
Q	y	4141	CCCTGGATGTACAAAGACAGTACACATTTGCACCATGATGCTCTGAGGACACGGGA	4200
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Q	y	4201	ACCTTGAACCTTTAAAGCCCTTCACAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4260
D	b	4201	ACCTTGAACCTTTAAAGCCCTTCACAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4260
Q	y	4261	GGAAACCAATCCAGACACAGCCCTGCCAGCGAGGGGAGGAAGTGGACACTGSCCCCA	4320
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Q	y	4321	GTTCCTCCAGACCATATGACCTCTTCCAGATGGGAATGGCAATGCAGAACCCCTTCA	4380
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Qy	4681	CACCTAAAGCTGGCCAAAGGACAGTCTCGAGATCGATTCTCAACAGCTTGGGAAGATT	4740
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Qy	4981	GTCATCTTTTGGATATGTCCTGTCGCCAGCAGCTTTGCTGATATCTCTGATCCAGAGCGG	5040
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Qy	5041	GTCAGCAAGCAAAACACCTGCAATTCATCAGTGAGTGAAGCCTGTCTACTGGCTC	5100
Db	5041	GTCAGCAAGCAAAACACCTGCAATTCATCAGTGAGTGAAGCCTGTCTACTGGCTC	5100
Qy	5101	TCTAATTTTGTCTGGGATATGTCGATTCAGTTGCTTCCTTGCACACATGGTGCAATTATCATC	5160
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Qy	5521	GTGTACCATTAATCTTGGGACTTTGGTGGGACGAAACCTCTTTCGCCATGCGCGTGGAAAGG	5580
Db	5521	GTGTACCATTAATCTTGGGACTTTGGTGGGACGAAACCTCTTTCGCCATGCGCGTGGAAAGG	5580
Qy	5581	GTGTGTCTCTCTCATTAATCTTCTGATCCAGTACAGATTTCTCATCAGGCCAGACCT	5640
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RESULT 11
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LOCUS AX127830
DEFINITION Sequence 69 from Patent WO0130848.
ACCESSION AX127830
VERSION AX127830.1 GI:14134477
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9741)
AUTHORS Benefie,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
TITLE Nucleic acids of the human abcl1 gene and their therapeutic and
diagnostic application
JOURNAL Patent: WO 0130848-A 69 03-MAY-2001;
FEATURES Location/Qualifiers
source 1. .9741

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ORIGIN									
Query Match	99.7%	Score 6764.8;	DB 6;	Length 9741;					
Best Local Similarity	99.8%	Pred. No. 0;							
Matches 6772;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps					
QY	1	ATGGCTTTGTTGGCTCAGCTGAGTGTCTGCTCTGGGAAGCACTCACTTTCAAGAAGA	60						
Db	185	ATGGCTTTGTTGGCTCAGCTGAGTGTCTGCTCTGGGAAGCACTCACTTTCAAGAAGA	244						
QY	61	CAAAATGTGAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCCTGATC	120						
Db	245	CAAAATGTGAGCTGCTGCTGGAAGTGGCTGGCTCTATTATCTTCTGATCCTGATC	304						
QY	121	TCTGTTCGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	180						
Db	305	TCTGTTCGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	364						
QY	181	ATGCCCTCTGCAGGAACACATTCCTTGGGTTTCAGGGGATATCTGTAAATGCCAAACGCC	240						
Db	365	ATGCCCTCTGCAGGAACACATTCCTTGGGTTTCAGGGGATATCTGTAAATGCCAAACGCC	424						
QY	241	TGTTTCGGTTACCCGAGCTCCTCGGGAGGCTCCCGGAGTGTGGTGGAAACATTTAACAAATCC	300						
Db	425	TGTTTCGGTTACCCGAGCTCCTGGGAGGCTCCCGGAGTGTGGTGGAAACATTTAACAAATCC	484						
QY	301	ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC	360						
Db	485	ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC	544						
QY	361	AGCATGAAGGACATGCGCAAGTCTTGAGAACATTTACAGCAGATCAAGAAATCCAGCTCA	420						
Db	545	AGCATGAAGGACATGCGCAAGTCTTGAGAACATTTACAGCAGATCAAGAAATCCAGCTCA	604						
QY	421	AACCTGAAGCTTCAAGATTTCCCTGGTGGCAATGAACCTTCTCTGGTTCCTATATACAC	480						
Db	605	AACCTGAAGCTTCAAGATTTCCCTGGTGGCAATGAACCTTCTCTGGTTCCTGATATCAC	664						
QY	481	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCAATCTCCAC	540						
Db	665	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCAATCTCCAC	724						
QY	541	AAGGTATTTTGAAGGCTACCAAGTTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA	600						
Db	725	AAGGTATTTTGAAGGCTACCAAGTTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA	784						
QY	601	GAAGAGATGATTTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	660						
Db	785	GAAGAGATGATTTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	844						
QY	561	AAACTGGCTGCAGCAGAGGAGTACTTCTGTTCCACATGGACATCCTGAAAGCAATCTGT	720						
Db	845	AAACTGGCTGCAGCAGAGGAGTACTTCTGTTCCACATGGACATCCTGAAAGCAATCTGT	904						
QY	721	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTGAAGCCACAAAACA	780						
Db	905	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAACA	964						
QY	781	TGCTGTCATAGTCTTGGGACTCTGGCCCAAGGAGCTGTTTTCAGCATGAGAGCTGGAGTGAC	840						
Db	965	TGCTGTCATAGTCTTGGGACTCTGGCCCAAGGAGCTGTTTTCAGCATGAGAGCTGGAGTGAC	1024						
QY	841	ATGCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC	900						
Db	1025	ATGCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC	1084						
QY	901	TACAGGCTGTGTCGTATTTCTTTCGCGGCATCCCGAGGAGGGGGCTGAAGATCAAG	960						
Db	1085	TACAGGCTGTGTCGTATTTCTTTCGCGGCATCCCGAGGAGGGGGCTGAAGATCAAG	1144						

QY	961	TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020
DB	1145	TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1204
QY	1021	GAAGATGCTGAAACCTTCTATGACAACTCTCAACTCTCTTACTGCAATGATTGATGAAG	1080
DB	1205	GAAGATGCTGAAACCTTCTATGACAACTCTCAACTCTCTTACTGCAATGATTGATGAAG	1264
QY	1081	AATTTGGAGTCTAGTCCCTCTTTCCCGCATTTATCTGGAAGCTCTGAAGCCGCTGCTCT	1140
DB	1265	AATTTGGAGTCTAGTCCCTCTTTCCCGCATTTATCTGGAAGCTCTGAAGCCGCTGCTCT	1324
QY	1141	GGGAAGATCCTGTATACACTGACACTCCAGCCACAAGCAGGTCATGCTGAGGTGAAC	1200
DB	1325	GGGAAGATCCTGTATACACTGACACTCCAGCCACAAGCAGGTCATGCTGAGGTGAAC	1384
QY	1201	AAGACTTCCAGGAACCTGCTGTTCATGATCTGGAAGGATGCTGGAGGAATCAAGC	1260
DB	1385	AAGACTTCCAGGAACCTGCTGTTCATGATCTGGAAGGATGCTGGAGGAATCAAGC	1444
QY	1261	CCCAAGATCTGAGCCTTCATGGAGAACCCCAAGAAATGGACCTTGTCCGGATGCTGTG	1320
DB	1445	CCCAAGATCTGAGCCTTCATGGAGAACCCCAAGAAATGGACCTTGTCCGGATGCTGTG	1504
QY	1321	GACACAGGGAACATGACCACTTTTGGGAACAGCAGTGTGGATGGCTTAGATTGGACGCC	1380
DB	1505	GACACAGGGAACATGACCACTTTTGGGAACAGCAGTGTGGATGGCTTAGATTGGACGCC	1564
QY	1381	CAAGACATCTGTCCTGCTTTTGGCCAAAGCAGCAGGATGCTCCAGTCCAGTAAATGGTCT	1440
DB	1565	CAAGACATCTGTCCTGCTTTTGGCCAAAGCAGCAGGATGCTCCAGTCCAGTAAATGGTCT	1624
QY	1441	GTGTACACTGAGAGAAAGCTTTCAACGAGACTTAACAGGCAATCCGAGCAATATCTCGC	1500
DB	1625	GTGTACACTGAGAGAAAGCTTTCAACGAGACTTAACAGGCAATCCGAGCAATATCTCGC	1684
QY	1501	TTCATGGAGTGTGCAACTGACAGCTAGAACCCATAGAACAGAGTGTGCTCATC	1560
DB	1685	TTCATGGAGTGTGCAACTGACAGCTAGAACCCATAGAACAGAGTGTGCTCATC	1744
QY	1561	AACAAAGTCCATGGAGTCTGCTGATGAGAGAAAGTCTGGGCTGCTATTGCTTCACTGGA	1620
DB	1745	AACAAAGTCCATGGAGTCTGCTGATGAGAGAAAGTCTGGGCTGCTATTGCTTCACTGGA	1804
QY	1621	ATTACTCCAGGAGGATGAGTCTGCCCATCATGTCAAGTACAAGATCCGAATGGACAT	1680
DB	1805	ATTACTCCAGGAGGATGAGTCTGCCCATCATGTCAAGTACAAGATCCGAATGGACAT	1864
QY	1681	GACAAATGAGAGGACAAATAAATAAAGGATGGTACTGGGACCTGTGCTCTGAGCT	1740
DB	1865	GACAAATGAGAGGACAAATAAATAAAGGATGGTACTGGGACCTGTGCTCTGAGCT	1924
QY	1741	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGCTTTCGCTACTTTCAGGATGTGGT	1800
DB	1925	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGCTTTCGCTACTTTCAGGATGTGGT	1984
QY	1801	GAGCAGCAATCATCAGGCTGCTGACGGGACCCAGAGAAACTGGTCTATATGCAA	1860
DB	1985	GAGCAGCAATCATCAGGCTGCTGACGGGACCCAGAGAAACTGGTCTATATGCAA	2044
QY	1861	CAGATGCCCTATCCCTGTAGCTTGTAGTACATCTTTCTGGGGTGTAGTCCGCTCAATG	1920
DB	2045	CAGATGCCCTATCCCTGTAGCTTGTAGTACATCTTTCTGGGGTGTAGTCCGCTCAATG	2104
QY	1921	CCCCTCTTCATGAGCTGGCTGATTTACTAGTGGCTGTGATCATCAAGGCAATCGT	1980
DB	2105	CCCCTCTTCATGAGCTGGCTGATTTACTAGTGGCTGTGATCATCAAGGCAATCGT	2164
QY	1981	TATGAGAGGAGGACCGCTGAAAGACCATCGGATCATGGCCCTGGGACACAGCATA	2040
DB	2165	TATGAGAGGAGGACCGCTGAAAGACCATCGGATCATGGCCCTGGGACACAGCATA	2224
QY	2041	CTCTGGTTTASCTGTTTCATAGTAGCTCATCTCTCTCTTCTTGTGAGCGCTGGCTGCTA	2100

Db	2225	 CTCTGTTAGTGGTTCATTAGTAGCCTCAATCCTCTCTCTTGTGAGCGGTGCCTGCTA	2284
Qy	2101	 GTGCTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCGACGCTGCTTTGTC	2160
Db	2285	 GTGCTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCGACGCTGCTTTGTC	2344
Qy	2161	 TTCTCTCCGCTGTTTCTGCTGGTGACAACTCTGCAAGTCTTCCTGATTAGCACACTCTTC	2220
Db	2345	 TTCTCTCCGCTGTTTCTGCTGGTGACAACTCTGCAAGTCTTCCTGATTAGCACACTCTTC	2404
Qy	2221	 TCAGAGCCAACTGSCAGACGCTGTGGGGGCATCATCTACTCTACGCTGATACCTGCCC	2280
Db	2405	 TCAGAGCCAACTGSCAGACGCTGTGGGGGCATCATCTACTCTACGCTGATACCTGCCC	2464
Qy	2281	 TAGCTCCTGTGTGGCATGGCAGACACTACGTGGGCTCTCACACTCAAGATCTTCGCTAGC	2340
Db	2465	 TAGCTCCTGTGTGGCATGGCAGACACTACGTGGGCTCTCACACTCAAGATCTTCGCTAGC	2524
Qy	2341	 CTGCTGTCTCTGTGGCTTTTGGCTGTGAGTACTTTGGCCTTTTGGAGGACGAG	2400
Db	2525	 CTGCTGTCTCTGTGGCTTTTGGCTGTGAGTACTTTGGCCTTTTGGAGGACGAG	2584
Qy	2401	 GGCATTGGAGTGCAGTGGGACAACTGTTGAGAGTCTCTGGGAGGAAGATGCTTCAAT	2460
Db	2585	 GGCATTGGAGTGCAGTGGGACAACTGTTGAGAGTCTCTGGGAGGAAGATGCTTCAAT	2644
Qy	2461	 CTCACCACHTCCGATPCCATGATGCTGTTGACACCTTCCCTATGSGGTGATGACCTGG	2520
Db	2645	 CTCACCACHTCCGCTPCCATGATGCTGTTGACACCTTCCCTATGSGGTGATGACCTGG	2704
Qy	2521	 TACATTGAGGCTGCTTTCCAGGCCAGTACGGAAATCCCGAGGCCCTGSTATTTTCTTTC	2580
Db	2705	 TACATTGAGGCTGCTTTCCAGGCCAGTACGGAAATCCCGAGGCCCTGSTATTTTCTTTC	2764
Qy	2581	 ACCAAGTCTCTACTGGTTTGGCGAGGAAAGTGATGAGAGAGCCACCCTGGTTCCAAACC	2640
Db	2765	 ACCAAGTCTCTACTGGTTTGGCGAGGAAAGTGATGAGAGAGCCACCCTGGTTCCAAACC	2824
Qy	2641	 AAGAGAATGTCAGAAATCTGCATGGAGGAGGNAACCCACCACCTTTGAAGCTGGGCGTGC	2700
Db	2825	 AAGAGAATGTCAGAAATCTGCATGGAGGAGGNAACCCACCACCTTTGAAGCTGGGCGTGC	2884
Qy	2701	 ATTCCAGAACCTCGTAAAGTCTACCGAGATGGGATGAAGTGGGTGCTGATGGCCTGGCA	2760
Db	2885	 ATTCCAGAACCTCGTAAAGTCTACCGAGATGGGATGAAGTGGGTGCTGATGGCCTGGCA	2944
Qy	2761	 CTGAATTTTTATGAGGCGCAGATCACCCTCTCTCTGGGCGACATGAGCGGGGAGAACG	2820
Db	2945	 CTGAATTTTTATGAGGCGCAGATCACCCTCTCTCTGGGCGACATGAGCGGGGAGAACG	3004
Qy	2821	 ACCACCATGTCAATCTGTACCGGGTGTGTCCCGCCGACCTCGGGCACCGCCTACATCCTG	2880
Db	3005	 ACCACCATGTCAATCTGTACCGGGTGTGTCCCGCCGACCTCGGGCACCGCCTACATCCTG	3064
Qy	2881	 GGAAAGACATTCGCTCTGAGATGAGCAACCATCCGGCGAGAACCTGGGGGTGTGTCCCCAG	2940
Db	3065	 GGAAAGACATTCGCTCTGAGATGAGCAACCATCCGGCGAGAACCTGGGGGTGTGTCCCCAG	3124
Qy	2941	 CATACGCTGCTGTTGACATGCTGACTGCTCGAGAGACATCTGTTCTATGCCCCGCTTG	3000
Db	3125	 CATACGCTGCTGTTGACATGCTGACTGCTCGAGAGACATCTGTTCTATGCCCCGCTTG	3184
Qy	3001	 AAAGGGTCTCTCAGAGACACGTGAAGCGCGAGATGGAGACAGATGGCCCTGGATGTTGGT	3060
Db	3185	 AAAGGGTCTCTCAGAGACACGTGAAGCGCGAGATGGAGACAGATGGCCCTGGATGTTGGT	3244
Qy	3061	 TTGCCATCAAGACGTGAAACCAAAACAAAGCGAGCTGTGAGTGGGAATGCAGAGAAG	3120
Db	3245	 TTGCCATCAAGACGTGAAACCAAAACAAAGCGAGCTGTGAGTGGGAATGCAGAGAAG	3304
Qy	3121	 CTATCTGTGGCCTTGGCTTTGTTCGGGGGATCTAAGGTGTCTATCTGGATGAACCCACA	3180

Db	3305	CTAFTCTGGCCCTTGGCCCTTTGTGGGGGATCTAAGGTTGTTCATCTGGGATGAACCCACA	3364
QY	3181	GCTGGTGTGACCCCTTACTCCGCGAGGGGAAATATGGGAGCTGCTGCTGAAATACCGACAA	3240
Db	3365	GCTGGTGTGACCCCTTACTCCGCGAGGGGAAATATGGGAGCTGCTGCTGAAATACCGACAA	3424
QY	3241	GGCGGCACCAATTATTCTCTCTACACACACATGGATGAAGCGGACGTCCTCGGGGACAGG	3300
Db	3425	GGCGGCACCAATTATTCTCTCTACACACACATGGATGAAGCGGACGTCCTCGGGGACAGG	3484
QY	3301	ATTGCCATCATCTCCCAATGGGAAGTGTGCTGTGTGGGCTCCTCCCTGTTTCTCAAGAAC	3360
Db	3485	ATTGCCATCATCTCCCAATGGGAAGTGTGCTGTGTGGGCTCCTCCCTGTTTCTCAAGAAC	3544
QY	3361	CAGCTGGGAACAGGCTACTACTGTGACCTTGGTCAAGAAGAATGTGGAAATCCTCCCTCAGT	3420
Db	3545	CAGCTGGGAACAGGCTACTACTGTGACCTTGGTCAAGAAGAATGTGGAAATCCTCCCTCAGT	3604
QY	3421	TCCTGCAAGAACAGTAGTAGCACTGTGTACACCTGAAAAGGAGGACAGTGTGTTCTCAG	3480
Db	3605	TCCTGCAAGAACAGTAGTAGCACTGTGTACACCTGAAAAGGAGGACAGTGTGTTCTCAG	3664
QY	3481	AGCAGTTCTGATCCTGCCCTGGGCGACGACCATGAGAGTGAACGCTGACCATCGATGTC	3540
Db	3665	AGCAGTTCTGATCCTGCCCTGGGCGACGACCATGAGAGTGAACGCTGACCATCGATGTC	3724
QY	3541	TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGGGAAGACATA	3600
Db	3725	TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGGGAAGACATA	3784
QY	3601	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAAGAGGGAGCCCTTTGTGAA	3660
Db	3785	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAAGAGGGAGCCCTTTGTGAA	3844
QY	3661	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCGATTTCTAGTTATGGCATCTCA	3720
Db	3845	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCGATTTCTAGTTATGGCATCTCA	3904
QY	3721	GAGACGACCCCTGGGAAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGCTGGATGCTGAG	3780
Db	3905	GAGACGACCCCTGGGAAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGCTGGATGCTGAG	3964
QY	3781	AGCTCAGATGTTACTTGGCCAGACAGACAGACAGCGGGGCTTCGGGGACACGACAGC	3840
Db	3965	AGCTCAGATGTTACTTGGCCAGACAGACAGACAGCGGGGCTTCGGGGACACGACAGC	4024
QY	3841	TGCTTTCGCCGTTCACTGGAAGATGATGCTGCTGATCCAAATGATTCAGATAGACCCA	3900
Db	4025	TGCTTTCGCCGTTCACTGGAAGATGATGCTGCTGATCCAAATGATTCAGATAGACCCA	4084
QY	3901	GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAAGGTCCTACAGGTGAAA	3960
Db	4085	GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAAGGTCCTACAGGTGAAA	4144
QY	3961	GGCTGGAAACTTACACAGACACAGTTTGTGGCCCTTTGCTGAAGAGACTGCTAAATGCC	4020
Db	4145	GGCTGGAAACTTACACAGACACAGTTTGTGGCCCTTTGCTGAAGAGACTGCTAAATGCC	4204
QY	4021	AGACGGAGTCGAAAGGATTTTGTCTCAGATTGTCTGCCAGCTGTGTTGTCTGTCATT	4080
Db	4205	AGACGGAGTCGAAAGGATTTTGTCTCAGATTGTCTGCCAGCTGTGTTGTCTGTCATT	4264
QY	4081	GGCCTTGTGTTACGCTGATCGTGCCACCTTTTGGCAAGTACCCACAGCGCTGGAACCTTCAG	4140
Db	4265	GGCCTTGTGTTACGCTGATCGTGCCACCTTTTGGCAAGTACCCACAGCGCTGGAACCTTCAG	4324
QY	4141	CCCTGGATGTACAAGAACAGTACACATTTGTCAAGCAATGATGCTCCTGAGGACACGGGA	4200
Db	4325	CCCTGGATGTACAAGAACAGTACACATTTGTCAAGCAATGATGCTCCTGAGGACACGGGA	4384
QY	4201	ACCCTGGAACTCTTAAAGCGCCCTACCAAAAGACCCCTGGGTCACCGCTGTATGGAA	4260
Db	4385	ACCCTGGAACTCTTAAAGCGCCCTACCAAAAGACCCCTGGGTCACCGCTGTATGGAA	4444

QY	4261	GGAAACCAATCCCGACACAGCCCTGCCAGGCGAGGGAGGAAGAGTGGACACTGCGCCCA	4320
Db	4445	GGAAACCAATCCCGACACAGCCCTGCCAGGCGAGGGAGGAAGAGTGGACACTGCGCCCA	4504
QY	4321	GTTCCTCCAGACCATCATGAGCCTCTTCCAGAAATGGGAAGTGGCAATGCAGAACCCCTTCA	4380
Db	4505	GTTCCTCCAGACCATCATGAGCCTCTTCCAGAAATGGGAAGTGGCAATGCAGAACCCCTTCA	4564
QY	4381	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGCCCCAGGG	4440
Db	4565	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGCCCCAGGG	4624
QY	4441	CGAGGGGGCTGCCTCTCTCCAAAGAAACAAAACACTGCAGATATCCCTTCAGGACCTG	4500
Db	4625	CGAGGGGGCTGCCTCTCTCCAAAGAAACAAAACACTGCAGATATCCCTTCAGGACCTG	4684
QY	4501	ACAGGAAGAAACATTTCCGGATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGC	4560
Db	4685	ACAGGAAGAAACATTTCCGGATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGC	4744
QY	4561	TTAAGAAACAGATCTGGGTGAATAGTTTAGTATGCGGCTTTTCCCTGGGTGTCAGT	4620
Db	4745	TTAAGAAACAGATCTGGGTGAATAGTTTAGTATGCGGCTTTTCCCTGGGTGTCAGT	4804
QY	4621	AATACTCAAGCACTTCCTCCGAGTCAGAAGTTAATGATGCCATCAACAATGAAGAA	4680
Db	4805	AATACTCAAGCACTTCCTCCGAGTCAGAAGTTAATGATGCCATCAACAATGAAGAA	4864
QY	4681	CACCTAAAGCTGGCCAAAGGACAGTTCTGCAGATCGATTCTCAACAGCTTGGCAAGATT	4740
Db	4865	CACCTAAAGCTGGCCAAAGGACAGTTCTGCAGATCGATTCTCAACAGCTTGGCAAGATT	4924
QY	4741	ATGCAGGACTGCACACCAAGAAATTAATGTCAAGGTGTGGTTCAATAACAAGGCTGGCAT	4800
Db	4925	ATGCAGGACTGCACACCAAGAAATTAATGTCAAGGTGTGGTTCAATAACAAGGCTGGCAT	4984
QY	4801	GCAATCAGCTCTTTCCCTGAAATGTCAATCAACATGCCATTCTCCGGGCGCAACCTGCAAAAG	4860
Db	4985	GCAATCAGCTCTTTCCCTGAAATGTCAATCAACATGCCATTCTCCGGGCGCAACCTGCAAAAG	5044
QY	4861	GGAGAAACCCTAGCAATTATGGAAATTAAGTCTCAATCAATCCCTGAAATCAACCAAG	4920
Db	5045	GGAGAAACCCTAGCAATTATGGAAATTAAGTCTCAATCAATCCCTGAAATCAACCAAG	5104
QY	4921	CAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGGATGTCTGTGTGTCATCTGT	4980
Db	5105	CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCTGTGTGTCATCTGT	5164
QY	4981	GTCAATCTTGCATATGTCCTTCTGCCAGCCAGCTTTGTCTGATTCCTGATCCAGGAGCGG	5040
Db	5165	GTCAATCTTGCATATGTCCTTCTGCCAGCCAGCTTTGTCTGATTCCTGATCCAGGAGCGG	5224
QY	5041	GTCAAGAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTCTCATCTACTTGGCTC	5100
Db	5225	GTCAAGAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTCTCATCTACTTGGCTC	5284
QY	5101	TCATAATTTGTCTGGGAATATGCGAATTAAGTTGTCCCTGCCACACTGGTCAATTATCATC	5160
Db	5285	TCATAATTTGTCTGGGAATATGCGAATTAAGTTGTCCCTGCCACACTGGTCAATTATCATC	5344
QY	5161	TTCAATCTGCTCCAGCAAGTCTATGTGTCTCCACCAATCTGCCTGTGTGTAGCCCTT	5220
Db	5345	TTCAATCTGCTCCAGCAAGTCTATGTGTCTCCACCAATCTGCCTGTGTGTAGCCCTT	5404
QY	5221	CTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTACCCAGCCCTCTTTGTGTTC	5280
Db	5405	CTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTACCCAGCCCTCTTTGTGTTC	5464
QY	5281	AGATTCCTCCAGCAGCCTATGTGGTGTCTACACAGGTGAACCTCTTATTTGGCAATTAA	5340
Db	5465	AGATTCCTCCAGCAGCCTATGTGGTGTCTACACAGGTGAACCTCTTATTTGGCAATTAA	5524

QY	5341	GGCAGCGTGGCCACCTTTGTGCTCGAGCTGTTCACGACAATAAGCTGAATTAATATCAAT	5400
Db	5525	GGCAGCGTGGCCACCTTTGTGCTCGAGCTGTTCACGACAATAAGCTGAATTAATATCAAT	5584
QY	5401	GATATCCTCGAAGTCGGTCTTTCATCTCCACATTTTGGCTGGGAGGCGTCATC	5460
Db	5585	GATATCCTCGAAGTCGGTCTTTCATCTCCACATTTTGGCTGGGAGGCGTCATC	5644
QY	5461	GACATGGTGA AAAACCAAGGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT	5520
Db	5645	GACATGGTGA AAAACCAAGGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT	5704
QY	5521	GTGTCCACCATATCTTGGGACTTGGTGGGAGCAAACTCTTGCCTAGCCGCGTGAAGGG	5580
Db	5705	GTGTCCACCATATCTTGGGACTTGGTGGGAGCAAACTCTTGCCTAGCCGCGTGAAGGG	5764
QY	5581	GTGGTGTTCCTTCCTCATCTGTTGATCCAGTACAGATTCTTCATCAGGCCACAGACCT	5640
Db	5765	GTGGTGTTCCTTCCTCATCTGTTGATCCAGTACAGATTCTTCATCAGGCCACAGACCT	5824
QY	5641	GTAATGCAAAAGCTATCTCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
Db	5825	GTAATGCAAAAGCTATCTCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5884
QY	5701	AGAATCTTGTGATGTGGAGCCAGAAATGACATCTTAGAANTCAAGAGGTTCACGAAGATA	5760
Db	5885	AGAATCTTGTGATGTGGAGCCAGAAATGACATCTTAGAANTCAAGAGGTTCACGAAGATA	5944
QY	5761	TATAGAAGAAAGCGGAAGCCTGCTGTGTGACAGGATTTGGTGGGCATTCCCTCGTGTGAG	5820
Db	5945	TATAGAAGAAAGCGGAAGCCTGCTGTGTGACAGGATTTGGTGGGCATTCCCTCGTGTGAG	6004
QY	5821	TGCTTTGGGCTCCGCGAGTTAATGGGCTGGAAATCATCAACTTTCAGATGTTTAAACA	5880
Db	6005	TGCTTTGGGCTCCGCGAGTTAATGGGCTGGAAATCATCAACTTTCAGATGTTTAAACA	6064
QY	5881	GGAGATACCAGCTGTTACCAGAGGAGATGCTTTCCCTTACAAAAATAGTATCTTATCAAC	5940
Db	6065	GGAGATACCAGCTGTTACCAGAGGAGATGCTTTCCCTTACAAAAATAGTATCTTATCAAC	6124
QY	5941	ATCCATGAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGCGTG	6000
Db	6125	ATCCATGAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGCGTG	6184
QY	6001	TTGACTGGGAGAACACGTTGGAGTTCTTTGGCCCTTTTGAGAGGAGTCCCACAGAAAAAA	6060
Db	6185	TTGACTGGGAGAACACGTTGGAGTTCTTTGGCCCTTTTGAGAGGAGTCCCACAGAAAAAA	6244
QY	6061	GTTGGCAGGTTGGTGAGTGGGCGATTCCGGAACCTGGGCCCTCGTGAAGTATGGAGAAAAA	6120
Db	6245	GTTGGCAGGTTGGTGAGTGGGCGATTCCGGAACCTGGGCCCTCGTGAAGTATGGAGAAAAA	6304
QY	6121	TATGCTGGTAACATATAGTGGAGCAACAAACCAAGCTCTCTACAGCCATGGCTTTCATC	6180
Db	6305	TATGCTGGTAACATATAGTGGAGCAACAAACCAAGCTCTCTACAGCCATGGCTTTCATC	6364
QY	6181	GGGGGCCCTCCTGTTGTTTCTGATGAACCCACAGGCATGGATCCCAAGACCCCG	6240
Db	6365	GGGGGCCCTCCTGTTGTTTCTGATGAACCCACAGGCATGGATCCCAAGACCCCG	6424
QY	6241	CGGTTCTGTGGAAATGTGCCCTAAGTGTGTCAGGAGGGAGATCAGTAGTGCCTTACA	6300
Db	6425	CGGTTCTGTGGAAATGTGCCCTAAGTGTGTCAGGAGGGAGATCAGTAGTGCCTTACA	6484
QY	6301	TCTCATAGTATGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6360
Db	6485	TCTCATAGTATGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6544
QY	6361	AGGTTCAAGTCTGGCAGTCTCCAGCATCTAAAAAATAGGTTTGAGATGTTTATACA	6420
Db	6545	AGGTTCAAGTCTGGCAGTCTCCAGCATCTAAAAAATAGGTTTGAGATGTTTATACA	6604
QY	6421	ATAGTTGTACGATAGCAGGGTCCAAACCCGAGCCTGAAGCTGTCCAGGATTTCTTTTGA	6480

Db	6605	ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGAAGCTGTCCAGGATTTCTTTGGG	6664
Qy	6481	CTTGCAATTTCTGGAAGTGTCTAAAAAGAGAAACACCGGAACATGCTACAAATACCACTT	6540
Db	6665	CTTGCAATTTCTGGAAGTGTCTAAAAAGAGAAACACCGGAACATGCTACAAATACCACTT	6724
Qy	6541	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA	6600
Db	6725	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA	6784
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 9741) Denufle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfoos Iii, G.H., Renaley, A., Brewer, H.B. and Dean, M.		
TITLE	Nucleic acids of the human abcl gene and their therapeutic and diagnostic application		
JOURNAL	Patent: EP 1096012-A 69 02-MAY-2001;		
FEATURES	Aventis Pharma S.A. (Fr)		
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Qy	181	ATGCCCTCTGCAGGAACACTTCCCTTGGGTTCAGGGGATATCTGTAATGCCAACAAACCC	240
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P.,
 Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
 TITLE Regulatory nucleic acid sequences of the abcl gene
 JOURNAL Patent: WO 0183746-A 10 08-NOV-2001;
 Aventis Pharma S.A. (FR)
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RESULT 14
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source

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Sequence 70 from Patent WO0130848.
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AX127831.1 GI:14134478
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 9854)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguinne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
1. 9854
/organism="Homo sapiens"

BASE COUNT		/db_xref="taxon:9606"		2665 a 2219 c 2334 g 2635 t 1 others	
ORIGIN					
Query Match		99.7%; Score 6764.8; DB 6; Length 9854;			
Best Local Similarity		99.8%; Pred No. 0;			
Matches 6772; Conservative		0; Mismatches 12; Indels 0; Gaps 0;			
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Db	298	ATGGCTGTGGGCTCAGCTGAGTGTCTGCTGTGGAAGAACCTCCTCTTCAAGAAGA	357		
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Db	358	CAACATGTCAGCTGTACTGGAAGTGGCTGGCCCTATTATCTCTCTGATCTGATC	417		
QY	121	TCGTGTGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCC	180		
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Db	1618	GACAGCAGGAGCAATGACCACTTTTGGGAACAGCAGTGGATGGCTTAGATTGGACAGCC	1677		
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Db	1678	CAAGACATCTGTGGGCTTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAAATGGTTCT	1737		
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QY	2461	CTCACCACATTCGATCTCCATGATGCTG	TTGACACCTTCCTCTATGGGTGATGACCTGG	2520
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QY	2521	TACATTGAGGCTGTCTTTCCAGGCCAG	TACGGAATTCOCAGGCCCTGGTATTTTCCCTTC	2580
Db	2818	TACATTGAGGCTGTCTTTCCAGGCCAG	TACGGAATTCOCAGGCCCTGGTATTTTCCCTTC	2877
QY	2581	ACCAAGTCTCTACTGTTTGGCGAGGAA	AGTATGAGAGAGCCACCTGGTTCACACCAG	2640
Db	2878	ACCAAGTCTCTACTGTTTGGCGAGGAA	AGTATGAGAGAGCCACCTGGTTCACACCAG	2937
QY	2641	AAGAGAAATGTCAAAATCTGCATGGAG	GAGGAACCCACCTTTGAAGCTGGCGTGCTCC	2700
Db	2938	AAGAGAAATGTCAAAATCTGCATGGAG	GAGGAACCCACCTTTGAAGCTGGCGTGCTCC	2997
QY	2701	ATTTCAGAACCTGGTAAAGTCTACCGAG	ATGGGATGGAGTGGCTGTGCATGGCCTGGCA	2760
Db	2998	ATTTCAGAACCTGGTAAAGTCTACCGAG	ATGGGATGGAGTGGCTGTGCATGGCCTGGCA	3057
QY	2761	CTGAATTTTATGAGGGCCAGATCACTCT	TCCTTGGGCCACAAATGGAGCGGGGAAGACG	2820
Db	3058	CTGAATTTTATGAGGGCCAGATCACTCT	TCCTTGGGCCACAAATGGAGCGGGGAAGACG	3117
QY	2821	ACCACCATGTCAATCTGCACCGGGTGT	TCCCCCGACCTCGGGACCGCCTACATCCTG	2880
Db	3118	ACCACCATGTCAATCTGCACCGGGTGT	TCCCCCGACCTCGGGACCGCCTACATCCTG	3177
QY	2881	GGAAAAGACATTCGCTCTCAGATGAG	CACCACTCCGGCAGAACCTTGGGGGTCTGTCC	2940
Db	3178	GGAAAAGACATTCGCTCTCAGATGAG	CACCACTCCGGCAGAACCTTGGGGGTCTGTCC	3237
QY	2941	CATAAGCTGCTGTTTGACATGCTGACT	GTGTCGGAAGAACACATCTGGTGTCTATG	3000
Db	3238	CATAAGCTGCTGTTTGACATGCTGACT	GTGTCGGAAGAACACATCTGGTGTCTATG	3297
QY	3001	AAAGGGCTCTCTCAGAGACGATGAAG	CGGGAGATGGAGCAGATGGCCCTGGATGTGG	3060
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QY	3121	CTATCTGTGGCCTTTGGCCTTTTGTGG	GGGATCTAAGGTTGTCTCTGGATGAACCCACA	3180
Db	3418	CTATCTGTGGCCTTTGGCCTTTTGTGG	GGGATCTAAGGTTGTCTCTGGATGAACCCACA	3477

Qy	3181	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3240
Db	3478	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3537
Qy	3241	GGCGGCACCAATTATCTCTCTACACACACATGGATGAAGCGGACGTCCTGGGGGACAGG	3300
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Qy	3301	ATTGGCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTTGAGAAC	3360
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Qy	3481	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC	3540
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Qy	3721	GAGACGACCCCTGGAAGAAATATTCCTCAAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG	3780
Db	4018	GAGACGACCCCTGGAAGAAATATTCCTCAAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG	4077
Qy	3781	ACCTCAGATGGTACCTTGGCCAGACGAACACGCGGGCTTCGGGGACAACGACAGC	3840
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Qy	3901	GAATCCAGAGACAGACACTTGCTCAGTGGATGGATGGCAAGGTCCTACACAGTGAAA	3960
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Qy	4021	AGACGGAGTCGGAAGGATTTTTTGCTCAGATTGTCTGCCAGCTGTGTTTGTCTGCATT	4080
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ORGANISM Homo sapiens
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AUTHORS 1 (bases 1 to 9854)
Densfle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, Iii, G.H.,
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JOURNAL Patent: EP 1096012-A 70 02-MAY-2001;
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QY	3361	CAGCTGGGAACGGCTACTACTGACCTTGGTCAAGAAGATGTGGAATCCTCCCTCAGT	3420
Db	3658	CAGCTGGGAACGGCTACTACTGACCTTGGTCAAGAAGATGTGGAATCCTCCCTCAGT	3717
QY	3421	TCCTGCGAAGAACAGTAGTAGCACTGTGTCAATACCTGTAAGGAGGACAGTGTCTTCAG	3480
Db	3718	TCCTGCGAAGAACAGTAGTAGCACTGTGTCAATACCTGTAAGGAGGACAGTGTCTTCAG	3777
QY	3481	AGCAATTCATGCTCGGCTGGGACGACCATGAGATGAGTGCACGCTGACCATCGATGTC	3540
Db	3778	AGCAATTCATGCTCGGCTGGGACGACCATGAGATGAGTGCACGCTGACCATCGATGTC	3837

Db	5998	AGAAATCTTGGATGGTGGAGCCAGAAATGACATCTTAGAAATCAAGAGTTGACGAAGATA	6057
QY	5761	TATAGAAGGAAGCGGAAGCCTGCTGTGACAGGATTTGGTGGGCATCTCTCTGCTGGTGG	5820
Db	6058	TATAGAAGGAAGCGGAAGCCTGCTGTGACAGGATTTGGTGGGCATCTCTCTGCTGGTGG	6117
QY	5821	TGCTTTGGGCTCCTGGGAGTTAATGGGCTGGAAATCAATCAACTTCAAGATGTTACA	5880
Db	6118	TGCTTTGGGCTCCTGGGAGTTAATGGGCTGGAAATCAATCAACTTCAAGATGTTACA	6177
QY	5881	GGAGATACCACCTGTTACCAGAGAGATGTTCCCTTAACAAAAATAGTATCTATCAAAAC	5940
Db	6178	GGAGATACCACCTGTTACCAGAGAGATGTTCCCTTAACAAAAATAGTATCTATCAAAAC	6237
QY	5941	ATCCATGAAGTACATCAGAACTAGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6000
Db	6238	ATCCATGAAGTACATCAGAACTAGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6297
QY	6001	TTGACTGGGAGAGACACGCTGGAGTCTTTGGCCCTTTTGAGAGGAGTCCACAGAGAGAA	6060
Db	6298	TTGACTGGGAGAGACACGCTGGAGTCTTTGGCCCTTTTGAGAGGAGTCCACAGAGAGAA	6357
QY	6061	GTGGCAAGTTGGTGGAGTGGCGGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA	6120
Db	6358	GTGGCAAGTTGGTGGAGTGGCGGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA	6417
QY	6121	TATGCTGTAACTATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6418	TATGCTGTAACTATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGGCTTTGATC	6477
QY	6181	GGCGGCTCTCTGT	6240
Db	6478	GGCGGCTCTCTGT	6537
QY	6241	CGGTTCTGTGGAATGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT	6300
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QY	6301	TCTCATAGTATGGAAGATGTGAAGCTCTTGCATAGGATGGCAATCATGTCAATGGA	6360
Db	6598	TCTCATAGTATGGAAGATGTGAAGCTCTTGCATAGGATGGCAATCATGTCAATGGA	6657
QY	6361	AGGTTCCAGTGGCTGGAGTGTCCAGCATCTTAAATAAGTTTGGAGATGGTTATACA	6420
Db	6658	AGGTTCCAGTGGCTGGAGTGTCCAGCATCTTAAATAAGTTTGGAGATGGTTATACA	6717
QY	6421	ATAGTTGTACGAATAGCAGGTTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA	6480
Db	6718	ATAGTTGTACGAATAGCAGGTTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA	6777
QY	6481	CTTGCAATTTCTGGAAGTGTCCAAAGAGAAACACCGGAACATGCTACATACCAGCTT	6540
Db	6778	CTTGCAATTTCTGGAAGTGTCCAAAGAGAAACACCGGAACATGCTACATACCAGCTT	6837
QY	6541	CCATCTTCATATCTCTCTGGCAGGATATTACAGATCTCTCCAGAGCAAAAGCGA	6600
Db	6838	CCATCTTCATATCTCTCTGGCAGGATATTACAGATCTCTCCAGAGCAAAAGCGA	6897
QY	6601	CTCCACATAGAAGTACTCTGTTTCTCAGACAACTTGACCAAGTATTGTGAAGCTT	6660
Db	6898	CTCCACATAGAAGTACTCTGTTTCTCAGACAACTTGACCAAGTATTGTGAAGCTT	6957
QY	6661	GCCAAGGACCAAGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCAAGACA	6720
Db	6958	GCCAAGGACCAAGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCAAGACA	7017
QY	6721	GTAGTGGAGTGTGAGTCTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	6780
Db	7018	GTAGTGGAGTGTGAGTCTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	7077
QY	6781	GTAT 6784	

Db 7078 GTAT 7081

Search completed: April 3, 2003, 22:04:40
Job time : 13523.6 Secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 1141.31 Seconds
(without alignments)
13386.024 Million cell updates/sec

Title: US-09-595-526c-1_copy_291_7074

Perfect score: 6784

Sequence: 1 atgctgtgtggcctcagct.....agtgaagaagctatgtat 6784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6784	100.0	10442	22	AAF24680
2	6784	100.0	10442	22	AAF24702
3	6782.4	100.0	10474	22	AAF24685
4	6782.4	100.0	10474	22	AAF24686
5	6782.4	100.0	10474	22	AAF24707
6	6782.4	100.0	10474	22	AAF24708
7	6776	99.9	7860	22	AAF92835
8	6772.8	99.8	7860	22	AAF83826
9	6768	99.8	7260	22	AAD21326

10	6768	99.8	7260	22	AAI70315	Human ATP binding
11	6764.8	99.7	9741	22	AA506120	Human ABC1 DNA seq
12	6764.8	99.7	9741	24	AAD37273	Human ABC1 full-le
13	6764.8	99.7	9854	22	AA506121	Human ABC1 DNA seq
14	6763.2	99.7	7281	22	AAK51683	Human polynucleoti
15	6762.2	99.7	7086	22	ABA09200	Human ABCA1 homolo
16	6762.2	99.7	7086	22	AAK52667	Human polynucleoti
17	6742	99.4	7864	21	AAC69120	Human ABC1 choles
18	6740.4	99.4	7864	21	AAC69385	Human ABC1 choles
19	6740.4	99.4	7864	21	AAC69386	Human ABC1 choles
20	6740.4	99.4	7864	21	AAC69389	Human ABC1 choles
21	6726	99.1	7861	21	AAC69387	Human ABC1 choles
22	6718	99.0	7857	21	AAC69388	Human ABC1 choles
23	6708	98.9	6880	21	AAZ94734	Human ATP binding
24	6708	98.9	6880	22	AAI70314	Human ATP binding
25	6704.8	98.8	6880	22	AAD21325	Human ATP binding
26	1926.8	28.4	7323	21	AAZ94746	Human ATP binding
27	1926.8	28.4	7784	19	AAV33392	ATP binding cass
28	1904.4	28.1	5097	22	AAI93913	Human stomach can
29	1904.4	28.1	5097	22	AAH18233	Human ABCA7 sequ
30	1742.2	25.7	7795	24	ABL57810	Human ABCA7 codi
31	1737.4	25.6	6791	24	AAI44693	Human transporter
32	1735.8	25.6	6522	22	AA508706	Human PD-ATP-bind
33	1735.8	25.6	6768	24	AA519207	DNA encoding huma
34	1696	25.0	6607	22	AA54812	Nucleotide sequ
35	1531.6	22.6	5762	22	AA54792	Nucleotide sequ
36	1528.8	22.5	5811	22	AAD05626	Human secreted pro
37	1465	21.6	5669	22	AA508707	Human PD-ATP-bind
38	985	14.5	7610	24	AAD36299	Human transporter
39	985	14.5	8040	22	AA57452	Human ABCA2 transp
40	985	14.5	8195	22	AAH75187	Nucleotide sequ
41	985	14.5	8269	24	AAH53009	Human ATP binding
42	974.4	14.4	5540	24	AAD27271	Human transporter
43	953.6	14.1	6792	22	AAD02722	Human ATP binding
44	949.2	14.0	3437	23	AA573965	DNA encoding novel
45	949.2	14.0	4413	23	AA583715	DNA encoding novel

ALIGNMENTS

RESULT 1

AAF24680
ID AAF24680 standard; DNA; 10442 BP.

XX AAF24680;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of a human ABC1 polypeptide.

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 291..7076

FT FT /*tag= a

FT FT /product= "ABC1 polypeptide"

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

XX

Qy	1681	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGTGACTGGGACCCCTGGTCTCGAGCT	1740
Db	1971	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGTGACTGGGACCCCTGGTCTCGAGCT	2030
Qy	1741	GACCCCTTTGAGGACATCGGGTACGTCCTGGGGGGCTTCGCCCTACTGTCAGGATGTGGT	1800
Db	2031	GACCCCTTTGAGGACATCGGGTACGTCCTGGGGGGCTTCGCCCTACTGTCAGGATGTGGT	2090
Qy	1801	GAGCAGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGCTCTATATGCAA	1860
Db	2091	GAGCAGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGCTCTATATGCAA	2150
Qy	1861	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGGTGATGACCGGTCAATG	1920
Db	2151	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGGTGATGACCGGTCAATG	2210
Qy	1921	CCCTCTTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCGCATCGT	1980
Db	2211	CCCTCTTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCGCATCGT	2270
Qy	1981	TATGAGAGGAGCGCCGTGAAAGAGACCATCGGGATCATGGGCCCTGGACACACGCATA	2040
Db	2271	TATGAGAGGAGCGCCGTGAAAGAGACCATCGGGATCATGGGCCCTGGACACACGCATA	2330
Qy	2041	CTCTGGTTTAGCTGGTTCATTAGTAGSCCTCATTCCTCTCTGTGAGCGCTGGCCCTGCTA	2100
Db	2331	CTCTGGTTTAGCTGGTTCATTAGTAGSCCTCATTCCTCTCTGTGAGCGCTGGCCCTGCTA	2390
Qy	2101	GTGTCATCTGAACTTAGAAACCTGTCGCCCTACAGTGATCCACGCTGGTGTGTTGTC	2160
Db	2391	GTGTCATCTGAACTTAGAAACCTGTCGCCCTACAGTGATCCACGCTGGTGTGTTGTC	2450
Qy	2161	TTCTGTCCGTGTTGCTGTGGTGTGACAACTCTCTGCACTGCTTCTCTGATTAGCACACTCTTC	2220
Db	2451	TTCTGTCCGTGTTGCTGTGGTGTGACAACTCTCTGCACTGCTTCTCTGATTAGCACACTCTTC	2510
Qy	2221	TCCAGAGCCAACTGGCAGCAGCGCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCC	2280
Db	2511	TCCAGAGCCAACTGGCAGCAGCGCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCC	2370
Qy	2281	TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2571	TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2630
Qy	2341	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGGCTTTCCTTTTGGAGGACG	2400
Db	2631	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGGCTTTCCTTTTGGAGGACG	2690
Qy	2401	GGCATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2460
Db	2691	GGCATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2750
Qy	2461	CTCACCACTTCGATCTCCATGATGCTTTTGACACCTTCCCTCTATGGGGTGATGACCTGG	2520
Db	2751	CTCACCACTTCGATCTCCATGATGCTTTTGACACCTTCCCTCTATGGGGTGATGACCTGG	2810
Qy	2521	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAAATCCACGGCCCTGGTATTTTCCCTGTC	2580
Db	2811	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAAATCCACGGCCCTGGTATTTTCCCTGTC	2870
Qy	2581	ACCAAGTCTCTACTGGTTTGGCGAGGAAATGATGAGAGAGCCACCTGGTTCACACCCAG	2640
Db	2871	ACCAAGTCTCTACTGGTTTGGCGAGGAAATGATGAGAGAGCCACCTGGTTCACACCCAG	2930
Qy	2641	AAGAGAATGTCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2700
Db	2931	AAGAGAATGTCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2990
Qy	2701	ATTCAGAACCTGGTAAAGTCTACACAGATGGATGAGGTGGCTGTGCTGATGGCCTGGCA	2760
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DB	3171	GGAAAGACATTCGCTCTGAGATGAGCACCATCCGCGAGAACCTGGGGTCTGTCCCCAG	3230
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DB	3231	CATAAGGTGCTGTTGACATGCTGACTGTCGAAGACACATCTGTTCTTATCCCGCTTG	3290
QY	3001	AAAGGGCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGSCCTGGATGTGTG	3060
DB	3291	AAAGGGCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGSCCTGGATGTGTG	3350
QY	3061	TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGATGCAGAGAAAG	3120
DB	3351	TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGATGCAGAGAAAG	3410
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QY	3181	GCTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA	3240
DB	3471	GCTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA	3530
QY	3241	GGCCGACCATTAATCTCTCTACACACCATGATGAAGCGGACGCTCTGGGGGACAGG	3300
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DB	3591	ATTGCCATCATCTCCCATGGGAAGCTGTCTGTGGGCTCTCTCCCTGTTTCTGAAAGAC	3650
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QY	3421	TCCTGCAGAAACAGTAGTAGCACTGTGTATACCTCTGAAAAGGAGGACAGTGTTCCTCAG	3480
DB	3711	TCCTGCAGAAACAGTAGTAGCACTGTGTATACCTCTGAAAAGGAGGACAGTGTTCCTCAG	3770
QY	3481	AGCAGTTCTGATGCTGGCCTGGCAGCGACCATGAGATGACACGCTGACCATCGATGTC	3540
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QY	3541	TTGTCTATCTCAACCTCATCAGAAAGCATGTGTCTGAAAGCCCGGCTGTGTGGAAGACATA	3600
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DB	3891	GGGCATGAGTGACCTATGTGCTGCATATGAAGCTGCTTAAGGAGGGAGCCTTTGTGGAA	3950
QY	3661	CTCTTTTCATGAGATTGATGACCGGCTCTACAGCTGGCATTTTCTAGTTATGGCATCTCA	3720
DB	3951	CTCTTTTCATGAGATTGATGACCGGCTCTACAGCTGGCATTTTCTAGTTATGGCATCTCA	4010
QY	3721	GAGACGACCTTGAAGAAATATTTCCTCAAGGTGGCCGAGAGAGTGGGTGGATGTGTGAG	3780
DB	4011	GAGACGACCTTGAAGAAATATTTCCTCAAGGTGGCCGAGAGAGTGGGTGGATGTGTGAG	4070
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Db 5391 TCTAATTTTGTCTGGATATGTGCAATTTACGTTGTCCTGCCACACTGGTCATTTATCATC 5450
QY 5161 TTCATCTGCTTCCAGCAGAGTCTTATGTGTCTCCACCAATCTGCTGTGCTAGCCCTT 5220
Db 5451 TTCATCTGCTTCCAGCAGAGTCTTATGTGTCTCCACCAATCTGCTGTGCTAGCCCTT 5510
QY 5221 CTACTTTTGTCTGATGGTGTGTCATCACACTCTCATGTACCCAGCTCTCTTGTGCTTC 5280
Db 5511 CTACTTTTGTCTGATGGTGTGTCATCACACTCTCATGTACCCAGCTCTCTTGTGCTTC 5570
QY 5281 AAGATCCCAAGCAGCAGCTTATGTGGTGTCTCACAGCTGAACTCTTTCATTTGCCATTAAT 5340
Db 5571 AAGATCCCAAGCAGCAGCTTATGTGGTGTCTCACAGCTGAACTCTTTCATTTGCCATTAAT 5630
QY 5341 GGCAGCTGGCCACCTTTGTCTGAGCTGTTCACCCGACATAGCTGAATAATATCAAT 5400
Db 5631 GGCAGCTGGCCACCTTTGTCTGAGCTGTTCACCCGACATAGCTGAATAATATCAAT 5690
QY 5401 GATATCTCTGAAGTCCGTGTCTTGTGATCTTCCACATTTTTCCTGGACAGGGCTCATC 5460
Db 5691 GATATCTCTGAAGTCCGTGTCTTGTGATCTTCCACATTTTTCCTGGACAGGGCTCATC 5750
QY 5461 GACATGTGAAACACAGGCAATGGCTGATGCCCTGAAAGGTTTGGGGAGATCCGCTT 5520
Db 5751 GACATGTGAAACACAGGCAATGGCTGATGCCCTGAAAGGTTTGGGGAGATCCGCTT 5810
QY 5521 GTGTCACCATTTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATTCGCCGTTGAAGGG 5580
Db 5811 GTGTCACCATTTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATTCGCCGTTGAAGGG 5870
QY 5581 GTGCTGTCTTCTCTCATCTACTGTCTCATCCAGTACAGATCTTTCATCAGGCCACACCT 5640
Db 5871 GTGCTGTCTTCTCTCATCTACTGTCTCATCCAGTACAGATCTTTCATCAGGCCACACCT 5930
QY 5641 GTAAATGCAAGCTATCTCTCTGAATGATGAAGATGAAGATGTGAGGGCGGGAAGACAG 5700
Db 5931 GTAAATGCAAGCTATCTCTCTGAATGATGAAGATGAAGATGTGAGGGCGGGAAGACAG 5990
QY 5701 AGAATTTCTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGATTTGACAGAGATA 5760
Db 5991 AGAATTTCTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGATTTGACAGAGATA 6050
QY 5761 TATAGAAGGAAGCGGAAGCTGCTTGTGACAGATTTTCCGTGGGCTTCCTCTCTGTTGAG 5820
Db 6051 TATAGAAGGAAGCGGAAGCTGCTTGTGACAGATTTTCCGTGGGCTTCCTCTCTGTTGAG 6110
QY 5821 TGCTTTGGGCTCTGGAGTTAATGGGCTTGAATAATCATCAACTTTCAAGATGTTTAAACA 5880
Db 6111 TGCTTTGGGCTCTGGAGTTAATGGGCTTGAATAATCATCAACTTTCAAGATGTTTAAACA 6170
QY 5881 GGAGATACCACTGTACAGAGGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 5940
Db 6171 GGAGATACCACTGTACAGAGGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 6230
QY 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
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QY 6001 TTGACTGGGAGAACACCGTGGAGTCTTGTGCTCTTTGAGAGGAGTCCAGAGAGAA 6060
Db 6291 TTGACTGGGAGAACACCGTGGAGTCTTGTGCTCTTTGAGAGGAGTCCAGAGAGAA 6350

QY	6061	GTTTGGCAAGTTGGTGGAGTGGCGGATTCGGAAACTGGGCCCTCGTGAAGTATGGAGAAAAA	6120
Db	6351	GTTTGGCAAGTTGGTGGAGTGGCGGATTCGGAAACTGGGCCCTCGTGAAGTATGGAGAAAAA	6410
QY	6121	TATGCTGCTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6411	TATGCTGCTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6470
QY	6181	GGCGGCCCTCTGTGGTGTTCCTGGATGAACCCACCACAGGCATGGATCCCAAGCCCGG	6240
Db	6471	GGCGGCCCTCTGTGGTGTTCCTGGATGAACCCACCACAGGCATGGATCCCAAGCCCGG	6530
QY	6241	CGGTTCTCTGCAATGTGCCCCCTAAGTCTGTCTCAGGAGGGAGATCAGTAGTCCTTACA	6300
Db	6531	CGGTTCTCTGCAATGTGCCCCCTAAGTCTGTCTCAGGAGGGAGATCAGTAGTCCTTACA	6590
QY	6301	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAATGGA	6360
Db	6591	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAATGGA	6650
QY	6361	AGGTTCCAGTGGCCTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6420
Db	6651	AGGTTCCAGTGGCCTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6710
QY	6421	ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGGATTTCTTTGGA	6480
Db	6711	ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGGATTTCTTTGGA	6770
QY	6481	CTTTGCATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACAAATACCACTT	6540
Db	6771	CTTTGCATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACAAATACCACTT	6830
QY	6541	CCATCTTCATATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6600
Db	6831	CCATCTTCATATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6890
QY	6601	CTCCACATAGAAGACTACTCTCTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT	6660
Db	6891	CTCCACATAGAAGACTACTCTCTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT	6950
QY	6661	GCCAAAGCACAAGTGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCAACA	6720
Db	6951	GCCAAAGCACAAGTGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCAACA	7010
QY	6721	GTAGTGGAGGTTGCAGTTCTTCACATCTTTCTTACAGGATGAGAAGTGAAAAGAAAGCTAT	6780
Db	7011	GTAGTGGAGGTTGCAGTTCTTCACATCTTTCTTACAGGATGAGAAGTGAAAAGAAAGCTAT	7070
QY	6781	GTAT 5784	
Db	7071	GTAT 7074	

RESULT 2	
AAF24702	
ID	AAF24702 standard; DNA; 10442 BP.
XX	
XX	AAF24702;
XX	AC
XX	AC
DT	20-APR-2001 (first entry)
DE	Nucleotide sequence of a human ABC1 polypeptide.
XX	
XX	Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW	chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW	atherosclerosis; cholesterol transport; ss.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	291..7076
CDS	

FT	/*tag= a
FT	/product= "ABCl polypeptide"
XX	
XX	WO200078971-A2.
XX	
PD	28-DEC-2000.
XX	
XX	16-JUN-2000; 2000WO-US16591.
PF	
XX	18-JUN-1999; 99US-0140264.
XX	
PR	14-SEP-1999; 99US-0153872.
PR	19-NOV-1999; 99US-0166573.
XX	
XX	(CVTH-) CV THERAPEUTICS INC.
PA	(UNIW) UNIV WASHINGTON.
XX	
XX	Lawn RM, Wade D, Oram JF, Garvin M;
PI	
XX	WPI; 2001-137811/14.
DR	P-PSDB; AAB31365.
DR	
XX	
FT	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
FT	polynucleotides and polypeptides, useful for treatment of heart disease
PT	and other disorders associated with hypercholesterolemia and
PT	atherosclerosis -
XX	
XX	Claim 3; Page 117-123; 211pp; English.
PS	
XX	
CC	The present sequence encodes a human adenosine triphosphate (ATP)
CC	binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC	membranes and utilizes ATP hydrolysis to transport a wide variety of
CC	substrates across the plasma membrane. ABC1 is a pivotal protein in
CC	the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC	stores. ABC1 is defective in Tangier disease, a genetic disorder
CC	characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC	localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC	useful for developing pharmaceutical agents for the treatment of heart
CC	disease and other disorders associated with hypercholesterolemia and
CC	atherosclerosis. The genes are useful for developing screening assays to
CC	screen for compounds that regulate the expression of genes associated
CC	with cholesterol transport. The genes and proteins are also useful for
CC	are also useful as diagnostic indicators of cardiovascular disease and
CC	other disorders associated with hypercholesterolemia.
XX	
XX	Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other
XX	

	Query Match	100.0%;	Score 6784;	DB 22;	Length 10442;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 6784;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	ATGCGTTGTTGGCCCTCAGCTCAGGTTGCTGCTGTGGAGACCTTCATCTTCAGAGAGA	60			
Db	291	ATGCGTTGTTGGCCCTCAGCTCAGGTTGCTGCTGTGGAGAACCTTCATCTTCAGAGAGA	350			
Qy	61	CAAAACATGTCAGCTGTTACTGGAAAGTGGCCGTGGCCTCTATTATCTTCCTGATCCTGATC	120			
Db	351	CAACATGTCAGCTGTTACTGGAAAGTGGCCGTGGCCTCTATTATCTTCCTGATCCTGATC	410			
Qy	121	TCTGTGGCGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	180			
Db	411	TCTGTGGCGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	470			
Qy	181	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTCTAATGCCAACAAACCCC	240			
Db	471	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTCTAATGCCAACAAACCCC	530			
Qy	241	TGTTTCCGTTTACCGGACTCCTTGGGAGGCTCCCGGAGTTGTTGGAACACTTTAACAAAATCC	300			
Db	531	TGTTTCCGTTTACCGGACTCCTTGGGAGGCTCCCGGAGTTGTTGGAACACTTTAACAAAATCC	590			
Qy	301	ATTGTGGCTCGCGCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACGCCAGAAAGACACC	360			
Db	591	ATTGTGGCTCGCGCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACGCCAGAAAGACACC	650			

QY 361 AGCATGAAGACATGCGCAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 420
 Db 651 AGCATGAAGACATGCGCAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 710
 QY 421 AACTTGAAGCTTCAAGATTTCTCGTGGACAAATGAACCTTCTCTGGGTTCCCTATATCAC 480
 Db 711 AACTTGAAGCTTCAAGATTTCTCGTGGACAAATGAACCTTCTCTGGGTTCCCTATATCAC 770
 QY 481 AACTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGCTGATGTCATCTCCAC 540
 Db 771 AACTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGCTGATGTCATCTCCAC 830
 QY 541 AAGTATTTTGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
 Db 831 AAGTATTTTGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 890
 QY 601 GAAGAGATGATTAACCTTGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAGAGGAG 660
 Db 891 GAAGAGATGATTAACCTTGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAGAGGAG 950
 QY 661 AACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAAATGACATCCTGAAGCCCAATCCCTG 720
 Db 951 AACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAAATGACATCCTGAAGCCCAATCCCTG 1010
 QY 721 AGAACCTAACTCTAGATCTCCCTTCCCGAGCAAGAGGCTGGCTGAAGCCCAAAAAACA 780
 Db 1011 AGAACCTAACTCTAGATCTCCCTTCCCGAGCAAGAGGCTGGCTGAAGCCCAAAAAACA 1070
 QY 781 TTGCTGATAGTTTGGGACTCTGGCCAGGAGCTGTTGACGATGAGAGCTGGAGTGAC 840
 Db 1071 TTGCTGATAGTTTGGGACTCTGGCCAGGAGCTGTTGACGATGAGAGCTGGAGTGAC 1130
 QY 841 ATGGCAGCAGAGGTGATGTTTCTGACCAATGTAACAGCTCCAGCTCTCCACCCAAATC 900
 Db 1131 ATGGCAGCAGAGGTGATGTTTCTGACCAATGTAACAGCTCCAGCTCTCCACCCAAATC 1190
 QY 901 TACCAGCTGTGCTGATGTTGCTGGGCACTCCGAGGAGGGGGGCTGAAGATCAAG 960
 Db 1191 TACCAGCTGTGCTGATGTTGCTGGGCACTCCGAGGAGGGGGGCTGAAGATCAAG 1250
 QY 961 TCTCTCAACTGGTATGAGGACAACTACAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
 Db 1251 TCTCTCAACTGGTATGAGGACAACTACAAGCCCTCTTTGGAGGCAATGGCACTGAG 1310
 QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1080
 Db 1311 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1370
 QY 1081 AATTTGGAGTCTAGTCTCTTTCCCGCAATATCTGGAAGGCTCTGAAGCCGCTGCTCGTT 1140
 Db 1371 AATTTGGAGTCTAGTCTCTTTCCCGCAATATCTGGAAGGCTCTGAAGCCGCTGCTCGTT 1430
 QY 1141 GGAAGATCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGGTGAAC 1200
 Db 1431 GGAAGATCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGGTGAAC 1490
 QY 1201 AAGACCTTCCAGGAATGGCTGTGTTCCATGATCTGGAAGGATGTTGGAGGAATCCAGC 1260
 Db 1491 AAGACCTTCCAGGAATGGCTGTGTTCCATGATCTGGAAGGATGTTGGAGGAATCCAGC 1550
 QY 1261 CCAAGATCTGGACCTTCAATGAGAACACGCCAAGAAATGGACCTTGTCCGGATGTTG 1320
 Db 1551 CCAAGATCTGGACCTTCAATGAGAACACGCCAAGAAATGGACCTTGTCCGGATGTTG 1610
 QY 1321 GACAGCAGGACAAATCACCACCTTTTGGGAACAGCAGTTGATGGCTTAGATTTGGACAGC 1380
 Db 1611 GACAGCAGGACAAATGACCACCTTTTGGGAACAGCAGTTGATGGCTTAGATTTGGACAGC 1670
 QY 1381 CAAGACATCTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1440
 Db 1671 CAAGACATCTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1730

QY 1441 GTGTACACCTTGAGAGAGCTTTTCAACGAGACTAACCGGCAATCCGAGCATATCTCGC 1500
 Db 1731 GTGTACACCTTGAGAGAGCTTTTCAACGAGACTAACCGGCAATCCGAGCATATCTCGC 1790
 QY 1501 TTCTGAGAGTGTCTCAACCTGAACCCATAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1560
 Db 1791 TTCTGAGAGTGTCTCAACCTGAACCCATAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1850
 QY 1561 ACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTCTGGCTGGTATTGTGTCTACTGGA 1620
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 QY 1621 AATTACTCCAGGACGATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT 1680
 Db 1911 AATTACTCCAGGACGATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT 1970
 QY 1681 GACAATGTGGAGGACGACAAATAAATCAAGATGGGTACTGGGACCCCTGTCTCGAGCT 1740
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 Db 2091 GAGCAGGCAATCATCAGGTTGCTGACGGGCAACGAGAGAAACTGTTCTATATGCAA 2150
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 Db 2151 CAGATGCCCTATCCCTGTTAGCTTGCATGACATCTTCTCGGGGTCATGACCGGTCATG 2210
 QY 1921 CCCCCTTTTCATGACGCTGGCCTGGATTTTACTCAGTGGCTGTGATCATCAAGGGCATGGT 1980
 Db 2211 CCCCCTTTTCATGACGCTGGCCTGGATTTTACTCAGTGGCTGTGATCATCAAGGGCATGGT 2270
 QY 1981 TATGAGAGGAGGACGCTGAAAGAGACCATGGGATCATGGGCTGGGCAACAGACATA 2040
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 QY 2401 GGCATTTGAGTGCAGTGGGCAACCTGTTTCAGAGTCTCTGTGGAGGAGATGGCTTCAAT 2460
 Db 2691 GGCATTTGAGTGCAGTGGGCAACCTGTTTCAGAGTCTCTGTGGAGGAGATGGCTTCAAT 2750
 QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTTCACACCTTCTCTATGGGGTGTACGCTGG 2520
 Db 2751 CTCACCACTTCGATCTCCATGATGCTGTTTTCACACCTTCTCTATGGGGTGTACGCTGG 2810
 QY 2521 TACATTTGAGGCTGTCTTTTCCAGGCCAGTACGGAATCCAGGCCCTCGTATTTCCTTGC 2580

Db 2811 TACATTGAGGCTGTCTTCCAGGCGCAGTACGGAAATCCCGAGCCCTGGTATTTCCCTTGC 2870
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Db 2871 ACCNAGTCCCTACTGTTTGGCGAGGAAAGTATGAGAAGAGCCACCCCTGGTTCCCAACAG 2930
QY 2641 AAGAGAAATGTCAGAAATCTGCATGAGAGGAGAACCCACCCACTTGAAGCTGGCGGTGCC 2700
Db 2931 AAGAGAAATGTCAGAAATCTGCATGAGAGGAGAACCCACCCACTTGAAGCTGGCGGTGCC 2990
QY 2701 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAGGTGGCTGTCGATGCCCTGGCA 2760
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Db 3111 ACCACATGCTAACTGCTACCGGGTGTTCGCCCGGACCTGGGACCGCTACATCTCTG 3170
QY 2881 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGAACCTGGGGTCTGTCCCCAG 2940
Db 3171 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGAACCTGGGGTCTGTCCCCAG 3230
QY 2941 CATACGCTGCTGTTGACATGCTGACTGTCGAGACACATCTGTTCTATGCCCTCTG 3000
Db 3231 CATACGCTGCTGTTGACATGCTGACTGTCGAGAACACATCTGGTCTATGCCCGCTG 3290
QY 3001 AAGGGCTCTCTGAGAGACACCTGAGGGGGAGATGGAGCAGATGGCCCTGGATGTTGT 3060
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QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGATGACAGAAAG 3120
Db 3351 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGATGACAGAAAG 3410
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QY 3481 AGCAGTTCGATGCTGGCCCTGGGAGGACCATGAGATGACACAGCTGACCATCGATGTC 3540
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Db 4011 GAGAGCACCTTGGAGAAATATCTCTAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 4070
QY 3781 ACCTCAGATGTTACCTTCCCAAGAGCAAGCAAGCGGGCTTTCGGGGCAACAGCAGAGC 3840
Db 4071 ACCTCAGATGTTACCTTCCCAAGAGCAAGCAAGCGGGCTTTCGGGGCAACAGCAGAGC 4130
QY 3841 TGTCTTCCCGCTTCACTTGAAGATGATCTGATCCAAATGATCTGACATAGACCCA 3900
Db 4131 TGTCTTCCCGCTTCACTTGAAGATGATCTGATCCAAATGATCTGACATAGACCCA 4190
QY 3901 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGGATGGCAAGGGTCTTACCAAGTGA 3960
Db 4191 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGGATGGCAAGGGTCTTACCAAGTGA 4250
QY 3961 GGCTGGAACTTACACAGACAGATTTGTGGCCCTTTTGTGGAAGAGACTGCTAATGGCC 4020
Db 4251 GGCTGGAACTTACACAGACAGATTTGTGGCCCTTTTGTGGAAGAGACTGCTAATGGCC 4310
QY 4021 AGACGGAGTCCGAAAGATTTTGTCTCAGATTTGTCTTCCAGCTGTGTTGTCTGCAAT 4080
Db 4311 AGACGGAGTCCGAAAGATTTTGTCTCAGATTTGTCTTCCAGCTGTGTTGTCTGCAAT 4370
QY 4081 GCCCTTGTGTTTCCAGCTGATGTCACCCCTTTTGGCAAGTACCCAGCCTGGAACTTCAG 4140
Db 4371 GCCCTTGTGTTTCCAGCTGATGTCACCCCTTTTGGCAAGTACCCAGCCTGGAACTTCAG 4430
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Db 4551 GGAACCCCAATCCCAAGACACCCCTTGGGACCCGCTGTATGGAA 4610
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Db 4611 GTTCCCCAGACCATCATGGACCTCTTCCAGATGGGAAATGGACAATGCAGAACCTTCA 4670
QY 4381 CCTGATGCCATGTAGACGACACAAATCAAGAGATGCTGCCCTGTGTGCCCCAGGG 4440
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QY 4441 GCAGGGGGCTGCCCTCCACAAAGAAACAAACACTGACAGATATCCTTCAGGACCTG 4500
Db 4731 GCAGGGGGCTGCCCTCCACAAAGAAACAAACACTGACAGATATCCTTCAGGACCTG 4790
QY 4501 ACAGGAAGAAACATTTCCGATTTATCTGGTGAAGAGATGTGTGCAGATCATAGCCAAAGC 4560
Db 4791 ACAGGAAGAAACATTTCCGATTTATCTGTTGAAGAGATGTGTGCAGATCATAGCCAAAGC 4850
QY 4561 TTAAGAAACAAGATCTGGGTGAATAGTATGGGGCTTTTCCCTGGGTGTCAGT 4620
Db 4851 TTAAGAAACAAGATCTGGGTGAATAGTATGGGGCTTTTCCCTGGGTGTCAGT 4910
QY 4621 AATACTCAAGCACTTCTCCGAGTCAAGAGTAAATGATGCCATCAACAAATGAAGAA 4680
Db 4911 AATACTCAAGCACTTCTCCGAGTCAAGAGTAAATGATGCCATCAACAAATGAAGAA 4970
QY 4681 CACCTTAAAGCTGGCCAAAGACAGTTCCTGAGATCGATTTCTCAACAGCTTGGGAAGATTT 4740
Db 4971 CACCTTAAAGCTGGCCAAAGACAGTTCCTGAGATCGATTTCTCAACAGCTTGGGAAGATTT 5030

QY 4741 ATGACAGGACTGGACACGAGAAATATATGTCAGAGTGTGGTTCAATAACAAAGGCTGGCAT 4800
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 QY 4801 GCAATCAGCTCTTCTGCTGAATGTCATCAACAATGCCATTCTCGGSCCAACCTGCAAAAG 4860
 Db 5091 GCAATCAGCTCTTCTGCTGAATGTCATCAACAATGCCATTCTCGGSCCAACCTGCAAAAG 5150
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 Db 5151 GGAGAAACCCCTAGCCATTATGAATTAATGCTTTCAATCATCCCTGAAATCTACCAAG 5210
 QY 4921 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTCGTCATCTGT 4980
 Db 5211 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTCGTCATCTGT 5270
 QY 4981 GTCATCTTTGCAATGCTTCGTCGCCAGCCAGCTTTGTCGTTATTCCTGATCCAGAGGG 5040
 Db 5271 GTCATCTTTGCAATGCTTCGTCGCCAGCCAGCTTTGTCGTTATTCCTGATCCAGAGGG 5330
 QY 5041 GTGAGAAAGCAACACCTGAGTTCATCAGTGGAGTGAAGCCCTGATCTACTGGCTC 5100
 Db 5331 GTGAGAAAGCAACACCTGAGTTCATCAGTGGAGTGAAGCCCTGATCTACTGGCTC 5390
 QY 5101 TCTAATTTTGTCTGGGATATGTCGAATACGTTGTCCCTGCCACACTGGTCATTATCATC 5160
 Db 5391 TCTAATTTTGTCTGGGATATGTCGAATACGTTGTCCCTGCCACACTGGTCATTATCATC 5450
 QY 5161 TTCATCTGCTCCAGCAGAGTCCCTATGTCCTCCACCAATCTGCTGTCGTCACCCCTT 5220
 Db 5451 TTCATCTGCTCCAGCAGAGTCCCTATGTCCTCCACCAATCTGCTGTCGTCACCCCTT 5510
 QY 5221 CTACTTTTGTCTGAGTGGTCAATCAACACTCTCATGTACCCAGCTCTCTTTGTCGTC 5280
 Db 5511 CTACTTTTGTCTGAGTGGTCAATCAACACTCTCATGTACCCAGCTCTCTTTGTCGTC 5570
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 QY 5341 GGCAGCGTGGCCACCTTTGTCGTCAGCTGTCACCGCAATTAAGCTCAATTAATCAAT 5400
 Db 5631 GGCAGCGTGGCCACCTTTGTCGTCAGCTGTCACCGCAATTAAGCTCAATTAATCAAT 5690
 QY 5401 GATATCCTGAATCGCTGTTCTGTCATCTCCACATTTTTCGCTGGGACGAGGCTCATC 5460
 Db 5691 GATATCCTGAATCGCTGTTCTGTCATCTCCACATTTTTCGCTGGGACGAGGCTCATC 5750
 QY 5461 GACATGGTGAAGAACCCAGCAATGCTGATGCCCTGGAAGGTTTGGGAGAAATCGCTTT 5520
 Db 5751 GACATGGTGAAGAACCCAGCAATGCTGATGCCCTGGAAGGTTTGGGAGAAATCGCTTT 5810
 QY 5521 GTGTCACCAATTAATCTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGCTGGAAGG 5580
 Db 5811 GTGTCACCAATTAATCTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGCTGGAAGG 5870
 QY 5581 GTGGGTCTTCTCATTACTGTTCTGATCCAGTACAGATCTTCATCAGGCCACAGCTT 5640
 Db 5871 GTGGGTCTTCTCATTACTGTTCTGATCCAGTACAGATCTTCATCAGGCCACAGCTT 5930
 QY 5641 GTAAATGCAAGCTATCTCTCTGATGATGAAGTGAAGTGTGAGCGGGGAAAGACAG 5700
 Db 5931 GTAAATGCAAGCTATCTCTCTGATGATGAAGTGAAGTGTGAGCGGGGAAAGACAG 5990
 QY 5701 AGAATCTTGATGTTGGAGGCGCAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5760
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QY 5821 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAATAATCATCAACTTTCAAGATGTTAACA 5880
 Db 6111 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAATAATCATCAACTTTCAAGATGTTAACA 6170
 QY 5881 GGAGATCCACTGTTTACCAGAGGAGATGCTTCTTACAAAAATAGTATCTATCAAC 5940
 Db 6171 GGAGATCCACTGTTTACCAGAGGAGATGCTTCTTACAAAAATAGTATCTATCAAC 6230
 QY 5941 ATCCATGAAGTACATCAAGACATGGGCTACTGCCCTCAGTTTGTATGCATCAACAGAGCTG 6000
 Db 6231 ATCCATGAAGTACATCAAGACATGGGCTACTGCCCTCAGTTTGTATGCATCAACAGAGCTG 6290
 QY 6001 TTGACTGGGAGAGACAGCTGGAGTCTTTGCCCTTTTGGAGAGGATCCAGAGAAAGAA 6060
 Db 6291 TTGACTGGGAGAGACAGCTGGAGTCTTTGCCCTTTTGGAGAGGATCCAGAGAAAGAA 6350
 QY 6061 GTTGGCAAGGTTGGTGGGCGATTTCGGAACCTGGGCTCGTGAAGTATGGAGAAAA 6120
 Db 6351 GTTGGCAAGGTTGGTGGGCGATTTCGGAACCTGGGCTCGTGAAGTATGGAGAAAA 6410
 QY 6121 TATGCTGGTAACTATAGTGGAGGCAACAAAGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
 Db 6411 TATGCTGGTAACTATAGTGGAGGCAACAAAGCAAGCTCTCTACAGCCATGGCTTTGATC 6470
 QY 6181 GCGGGGCTCCTGTGGTGTCTGTGATGAACCCACACAGGATGGATCCCAAGCCCG 6240
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 QY 6241 CGGTTCTTGTGGAATGTGCCCTTAAGTGTGTCAAGGAGGGAGATCAGTAGTCTTACA 6300
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 QY 6301 TCTCATAGTATGGAAGTGTGAAGCTTTTGCATAGGATGCAATCATGGTCAATGGA 6360
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 QY 6361 AGTTTCAGGTGCTTGGCAGTGTCCAGCTATCAAAATAGTTTGGAGATGTTTATACA 6420
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 QY 6421 ATAGTCTGAGCAATAGCAGGTCACCCGAGCTGAGGCTGTCCAGGATTTCTTTGGA 6480
 Db 6711 ATAGTCTGAGCAATAGCAGGTCACCCGAGCTGAGGCTGTCCAGGATTTCTTTGGA 6770
 QY 6481 CTTCATTTCTTGGAGTGTCTTAAAGAGAAACACCCGAGCAATGCTTACAAATACCACTT 6540
 Db 6771 CTTCATTTCTTGGAGTGTCTTAAAGAGAAACACCCGAGCAATGCTTACAAATACCACTT 6830
 QY 6541 CCATCTTCATATCTTCTGCGCAGGATATTGAGCATCTCTCCAGAGCAAAAGCGA 6600
 Db 6831 CCATCTTCATATCTTCTGCGCAGGATATTGAGCATCTCTCCAGAGCAAAAGCGA 6890
 QY 6601 CTCACATAGAAGTACTCTGTCTTCAGCAACACTTGAACCAAGTATTGTGAACTTT 6660
 Db 6891 CTCACATAGAAGTACTCTGTCTTCAGCAACACTTGAACCAAGTATTGTGAACTTT 6950
 QY 6661 GCCAAGACCAAGTATGATGACCACTTAAAGAGCTCTCATTTACAAAAACCAAGACA 6720
 Db 6951 GCCAAGACCAAGTATGATGACCACTTAAAGAGCTCTCATTTACAAAAACCAAGACA 7010
 QY 6721 GTAGTGGACCTTGAGTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 6780
 Db 7011 GTAGTGGACCTTGAGTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 7070
 QY 6781 GTAT 6784
 Db 7071 GTAT 7074

AAF24685;
 20-APR-2001 (first entry)
 Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 Human; adenosine triphosphate binding cassette protein 1; ABC1;
 apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 chromosome 9q22-q31; heart disease; hypercholesterolemia;
 atherosclerosis; cholesterol transport; ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 323..7108
 /*tag= a
 /product= "defective ABC1 polypeptide"
 WO200078972-A2.
 28-DEC-2000.
 16-JUN-2000; 2000WO-US16765.
 18-JUN-1999; 99US-0140264.
 14-SEP-1999; 99US-0153872.
 19-NOV-1999; 99US-0166573.
 (CVTH-) CV THERAPEUTICS INC.
 Lawn RM, Wade D, Garvin M;
 WPI; 2001-137812/14.
 Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 useful for the development of agents for the treatment of heart disease
 and other disorders associated with hypercholesterolemia and
 atherosclerosis -
 Disclosure; Page 148-154; 215pp; English.
 The present sequence encodes a human adenosine triphosphate (ATP)
 binding cassette protein (ABC) 1 polypeptide, and is isolated from
 a Tangier disease patient. ABC1 resides in cell membranes and utilises
 ATP hydrolysis to transport a wide variety of substrates across the
 plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 mobilisation of intracellular cholesterol stores. ABC1 is defective in
 Tangier disease, a genetic disorder characterised by abnormal
 HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 9q22-q31. The ABC1 genes and proteins are useful for developing
 pharmaceutical agents for the treatment of heart disease and other
 disorders associated with hypercholesterolemia and atherosclerosis. The
 genes are useful for developing screening assays to screen for compounds
 that regulate the expression of genes associated with cholesterol
 transport. The genes and proteins are also useful for are also useful
 as diagnostic indicators of cardiovascular disease and other disorders
 associated with hypercholesterolemia.
 Sequence 10474 BP: 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
 Query Match 100.0%; Score 6782.4; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6793; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ATGGCTGTGGGCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGCTTCAGAAAGA 60
 323 ATGGCTGTGGGCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCAGCTTCAGAAAGA 382
 61 CAACAATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 120
 383 CAACAATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 442
 121 TCTGTTGGCTGAGTACCAACCCCTATGAACAACATGAATGCCATTTTCCAAATAAGCC 180

Db 443 TCTGTTGGCTGAGTACCAACCTATGAACAACATGAATGCCATTTTCCAAATAAGCC 502
 QY 181 ATGGCTGTGGGCTCAGGAACACATTCCTTGGGTTGAGGATATCTGTATGCAACAACCC 240
 Db 503 ATGGCTGTGGGCTCAGGAACACATTCCTTGGGTTGAGGATATCTGTATGCAACAACCC 562
 QY 241 TGTTCCTGTTACCGACATTCCTGGGAGGCTCCCGAGTGTGGAACTTTAAACAATCC 300
 Db 563 TGTTCCTGTTACCGACATTCCTGGGAGGCTCCCGAGTGTGGAACTTTAAACAATCC 622
 QY 301 ATTGTGGCTCGCTGTTCTCAGATGCTCGAGGCTCTCTTATACAGCAGAAAGACACC 360
 Db 623 ATTGTGGCTCGCTGTTCTCAGATGCTCGAGGCTCTCTTATACAGCAGAAAGACACC 682
 QY 361 AGCATGAAGGACATCGCAAAAGTTCTGAGACATTTACAGCAGATCAAGAAATCAGCTCA 420
 Db 683 AGCATGAAGGACATCGCAAAAGTTCTGAGACATTTACAGCAGATCAAGAAATCAGCTCA 742
 QY 421 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAAACCTTCTCTGGTCTCTATATCAC 480
 Db 743 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAAACCTTCTCTGGTCTCTATATCAC 802
 QY 481 AACTTCTCTCCAAAGTCTACTGTGACAAAGATGCTGAGGCTGAGTGTCTCTCCAC 540
 Db 803 AACTTCTCTCCAAAGTCTACTGTGACAAAGATGCTGAGGCTGAGTGTCTCTCCAC 862
 QY 541 AAGGTATTTTGAAGGCTACCAAGTTACATTTGACAACTCTGTGCAATGGATCAAAATCA 600
 Db 863 AAGGTATTTTGAAGGCTACCAAGTTACATTTGACAACTCTGTGCAATGGATCAAAATCA 922
 QY 601 GAAGAGATGATTCAACTTGGTGACCAAGATTTCTGAGCTTTGAGGCTTACCAAGGAG 560
 Db 923 GAAGAGATGATTCAACTTGGTGACCAAGATTTCTGAGCTTTGAGGCTTACCAAGGAG 982
 QY 661 AACTTGGCTGACAGAGAGAGTACTTCTGTTCCAACTGGACATCTCTGAAGCAATCTCTG 720
 Db 983 AACTTGGCTGACAGAGAGAGTACTTCTGTTCCAACTGGACATCTCTGAAGCAATCTCTG 1042
 QY 721 AGACACATAAATCTACATCTCCCTTCCGAGCAAGAGAGTGGCTGAAAGCCCAAAAACA 780
 Db 1043 AGACACATAAATCTACATCTCCCTTCCGAGCAAGAGAGTGGCTGAAAGCCCAAAAACA 1102
 QY 781 TTGCTGCATAGTCTTGGGACTCTGCCAGGAGCTGTTCCAGCATGAGAGCTGGAGTAC 840
 Db 1103 TTGCTGCATAGTCTTGGGACTCTGCCAGGAGCTGTTCCAGCATGAGAGCTGGAGTAC 1162
 QY 841 ATGCGACAGAGGCTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAATC 900
 Db 1163 ATGCGACAGAGGCTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAATC 1222
 QY 901 TACCAGGCTGTCTCGTATTGTTGCGGGCATCCGAGGAGGGGGCTGAGATCAAG 960
 Db 1223 TACCAGGCTGTCTCGTATTGTTGCGGGCATCCGAGGAGGGGGCTGAGATCAAG 1282
 QY 961 TCTCTCACTGTGTAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
 Db 1283 TCTCTCACTGTGTAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1342
 QY 1021 GAAGATGTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1080
 Db 1343 GAAGATGTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1402
 QY 1081 AATTGGAGCTGAGTCTCTTCCCGCATTTCTGAAAGCTCTGAAGCCGCTGCTCGTT 1140
 Db 1403 AATTGGAGCTGAGTCTCTTCCCGCATTTCTGAAAGCTCTGAAGCCGCTGCTCGTT 1462
 QY 1141 GGAAGATCTGTATACACTGACACTCCAGCCACAAGCAGGCTCATGGCTGAGTGAAC 1200
 Db 1463 GGAAGATCTGTATACACTGACACTCCAGCCACAAGCAGGCTCATGGCTGAGTGAAC 1522
 QY 1201 AGACCTTCCAGAACTGCTGTGTTCCATGATCTGGAAGGATGTGGAGGAACTCAGC 1260

Db 1523 AAGACCTTCCAGGAACCTGGCTGTCTCCATGATCTGGAAGGCAATGCGGAGGAACCTCAGC 1582
QY 1261 CCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGTCCGGATGCTGTG 1320
Db 1583 CCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGTCCGGATGCTGTG 1642
QY 1321 GACAGCAGGAGACAATGACCACTTTTGGAGAACAGCACTTGGATGGCTTAGATGGACAGCC 1380
Db 1643 GACAGCAGGAGACAATGACCACTTTTGGAGAACAGCACTTGGATGGCTTAGATGGACAGCC 1702
QY 1381 CAAGACATCGTGGCGTTTGGCCAAAGCACCCAGAGAGATGTCCAGTCCAGTAAATGGTTCT 1440
Db 1703 CAAGACATCGTGGCGTTTGGCCAAAGCACCCAGAGAGATGTCCAGTCCAGTAAATGGTTCT 1762
QY 1441 GTCTACACCTGGAGAGAGCTTTCACGAGAGATTAACAGGCAATCCGGACCAATATCTCGC 1500
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QY 1561 ACAAAGTCCATGGAGTGTCTGATGAGAGAAAGTCTTGGGCTGGTATGTTGTTCTACTGGA 1620
Db 1883 ACAAAGTCCATGGAGTGTCTGATGAGAGAAAGTCTTGGGCTGGTATGTTGTTCTACTGGA 1942
QY 1621 ATTACTCCAGGAGCAATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT 1680
Db 1943 ATTACTCCAGGAGCAATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT 2002
QY 1681 GACATGTGGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCCCTCGAGCT 1740
Db 2003 GACATGTGGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCCCTCGAGCT 2062
QY 1741 GACCCCTTTGAGACATGGGTGAGTCTGGGGGCTTCCGCTACTTCAGAGATGTTGG 1800
Db 2063 GACCCCTTTGAGACATGGGTGAGTCTGGGGGCTTCCGCTACTTCGGGATGTTGG 2122
QY 1801 GAGCAGGCAATCATCAGGCTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 1860
Db 2123 GAGCAGGCAATCATCAGGCTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 2182
QY 1861 CAGATCCCTATCCCTGTTCACCTTTCATGACATCTTTCGCGGCTGATGACGGCTCAATG 1920
Db 2183 CAGATGCCCTATCCCTGTTCACCTTTCATGACATCTTTCGCGGCTGATGACGGCTCAATG 2242
QY 1921 CCCCCTTTTCATGACCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGTG 1980
Db 2243 CCCCCTTTTCATGACCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGTG 2302
QY 1981 TATGAGAGGAGGACGCTGAAAGAGACCATGCGGATCATGGGCTGGAGCAACAGCAT 2040
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QY 2041 CTTCTGGTTAGCTGGTTTCAATAGTAGCTCAATTCCTCTTCTTGAGCGCTGGCTGCTA 2100
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Db 2423 GTGGTCACTGAAATAGGAACCTGTGCGCTACAGTATGCCAGCGTGGTGTGTC 2482
QY 2161 TTCTCTGTCGCTTGTGTGTGTGATCTCTGAGTGTCTTCTCTGATTAAGCAGCTCTTC 2220
Db 2483 TTCTCTGTCGCTTGTGTGTGTGATCTCTGAGTGTCTTCTCTGATTAAGCAGCTCTTC 2542
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QY 2341 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGGCTTTTGGAGAGCAG 2400
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QY 2401 GGCATTGGAGTGCAGTGGGCAACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTCAAT 2460
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QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGATGATCACCTGG 2520
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QY 2521 TACATTGAGGCTGTCTTTCAGGCCAGTACGGAATTCOCAGGCCCTGGTATTTTCCTTTC 2580
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QY 2641 AAGAGAATGTCAAGAAATCTGCATGGAGAGGAACCCACCCACTTTGAAGCTGGGCGTCTCC 2700
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QY 2701 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCTGGCA 2760
Db 3023 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCTGGCA 3082
QY 2761 CTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACCAATGAGCGGGGAGAGCG 2820
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QY 2881 GGAAGAGACATTCCTCTCTGAGATGAGCACCATCCGGCAGAACCTTGGGGCTCTGCCCAG 2940
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QY 3001 AAAGGGCTCTCTGAGAGCAGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT 3060
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QY 3061 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCAAGCAGCTGTCAGTGGATTCAGAGAAAG 3120
Db 3383 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCAAGCAGCTGTCAGTGGATTCAGAGAAAG 3442
QY 3121 CTATCTGTGGCTTGGCTTTGTGGGGGATCTAAGTGTCTCAATTCGATGAACCCACA 3180
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QY 3181 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAATACCCAGCAA 3240
Db 3503 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAATACCCAGCAA 3562
QY 3241 GGCGGACCACTTATCTCTACACACCATGATGAAGCGGACCTCTCTGGGGGACAGG 3300
Db 3563 GGCGGACCACTTATCTCTACACACCATGATGAAGCGGACCTCTCTGGGGGACAGG 3622
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Db 3623 ATTGCCATCATCTCCCATGGGAAAGCTGTGCTGTGGGCTCTCCCTGTTTCTGAAGAAC 3682
QY 3361 CAGCTGGGAGACGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3420
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QY	3421	TCCTGCAGAAAACAGTAGTAGCAGCTGTGTCTATACCTGAAAAGGAGGACAGTGTTCCTCAG	3480
Db	3743	TCCTGCAGAAAACAGTAGTAGCAGCTGTGTCTATACCTGAAAAGGAGGACAGTGTTCCTCAG	3802
QY	3481	AGCAGTTCTGATGCTGGCTGGCGACGACCATGAGAGTGCACGCTGACCATCGATGTC	3540
Db	3803	AGCAGTTCTGATGCTGGCTGGCGACGACCATGAGAGTGCACGCTGACCATCGATGTC	3862
QY	3541	TCCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGCTGGTGGGAAGACATA	3600
Db	3863	TCCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGCTGGTGGGAAGACATA	3922
QY	3601	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGCGCTTTGTGGAA	3660
Db	3923	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGCGCTTTGTGGAA	3982
QY	3661	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA	3720
Db	3983	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA	4042
QY	3721	GAGACAGCCCTGGAGAAATATTTCTCAAGTGGCCGAGAGAGTGGGTGGATGCTGAG	3780
Db	4043	GAGACAGCCCTGGAGAAATATTTCTCAAGTGGCCGAGAGAGTGGGTGGATGCTGAG	4102
QY	3781	ACCTCAGATGGTACCTTGGCCACAAGCAACAGCGCGGGCTTCGGGGACAAGCAGAGCG	3840
Db	4103	ACCTCAGATGGTACCTTGGCCACAAGCAACAGCGCGGGCTTCGGGGACAAGCAGAGCG	4162
QY	3841	TGTCCTCGCCGCTTCACTGAAGATGATGCTGTATGATCAAAATGATTTCTGACATAGACCCA	3900
Db	4163	TGTCCTCGCCGCTTCACTGAAGATGATGCTGTATGATCAAAATGATTTCTGACATAGACCCA	4222
QY	3901	GAATCCAGAGAGACAGACTGCTCAGTGGGATGGATGCAAGGGTCTCTACCAAGTGA	3960
Db	4223	GAATCCAGAGAGACAGACTGCTCAGTGGGATGGATGCAAGGGTCTCTACCAAGTGA	4282
QY	3961	GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAAGAGACTGCTAAATGGC	4020
Db	4283	GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAAGAGACTGCTAAATGGC	4342
QY	4021	AGACGGAGTCGGAAGAGATTTTTCCTCAGATTGCTTCCAGACTGTGTTGTCTGCATTT	4080
Db	4343	AGACGGAGTCGGAAGAGATTTTTCCTCAGATTGCTTCCAGACTGTGTTGTCTGCATTT	4402
QY	4081	GCCTCTGTGTTTCAGCCTGATCGTGCACCCCTTTGGCAAGTACCCACGCTGGAACTTCAG	4140
Db	4403	GCCTCTGTGTTTCAGCCTGATCGTGCACCCCTTTGGCAAGTACCCACGCTGGAACTTCAG	4462
QY	4141	CCCTGATGTACAAACAAACAGTACACATTTGTCACCAATGATGCTCTGAGGACACCGGA	4200
Db	4463	CCCTGATGTACAAACAAACAGTACACATTTGTCACCAATGATGCTCTGAGGACACCGGA	4522
QY	4201	ACCTTGGAACTCTTAAACGCCCTCACAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4260
Db	4523	ACCTTGGAACTCTTAAACGCCCTCACAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4582
QY	4261	GGAAACCCAAATCCGACAGCGCCCTGCCAGCGAGGGAGAGAGTGGACACTGCCOCCA	4320
Db	4583	GGAAACCCAAATCCGACAGCGCCCTGCCAGCGAGGGAGAGAGTGGACACTGCCOCCA	4642
QY	4321	GTTCGCCAGACCATATGAGACTCTTCCAGAATGGAACTGGACAAATGCAGAACCCCTTCA	4380
Db	4643	GTTCGCCAGACCATATGAGACTCTTCCAGAATGGAACTGGACAAATGCAGAACCCCTTCA	4702
QY	4381	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG	4440
Db	4703	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG	4762
QY	4441	GCAGGGGGCTGCTCCTCCACAAGAAACAAACACTGCAGATATCTCTTCAGACCTTG	4500
Db	4763	GCAGGGGGCTGCTCCTCCACAAGAAACAAACACTGCAGATATCTCTTCAGACCTTG	4822
QY	4501	ACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGCTATGTCCAGATCATAGCCAAAAGC	4560

Db	4823	ACAGGAAGAAACATTCGGATTATCTGTTGAAGACGTTATGTGCAGATCATAGCCAAAGC	4882
Qy	4561	TTAAAGAACAAAGATCTGGTGAATCAGTTTAGTTAGGTATGCGGCTTTTCCCTGGGTGTCAGT	4620
Db	4883	TTAAAGAACAAAGATCTGGTGAATCAGTTTAGTTAGGTATGCGGCTTTTCCCTGGGTGTCAGT	4942
Qy	4621	AATACTCAAGCACTTCCCTCCGAGTCAAGAAGTTTAATGATGCCATCAACAACAAATGAAGAAA	4680
Db	4943	AATACTCAAGCACTTCCCTCCGAGTCAAGAAGTTTAATGATGCCATCAACAACAAATGAAGAAA	5002
Qy	4681	CACCTAAAGCTGGCCAAAGGACAGTTCTCGAGATCGATTTCTCAACACGCTTGGGAAGATT	4740
Db	5003	CACCTAAAGCTGGCCAAAGGACAGTTCTCGAGATCGATTTCTCAACACGCTTGGGAAGATT	5062
Qy	4741	ATGACAGGACTGGACACCAAGAAATAATGTCGAAGGTGTGGTTTCAATAACAAGGCTGGCAT	4800
Db	5063	ATGACAGGACTGGACACCAAGAAATAATGTCGAAGGTGTGGTTTCAATAACAAGGCTGGCAT	5122
Qy	4801	GCATCAGCTCTTCTGTAATCTCATCAACAAATGCCATTCTCCGGGCCCAACCTGCAAAAAG	4860
Db	5123	GCATCAGCTCTTCTGTAATCTCATCAACAAATGCCATTCTCCGGGCCCAACCTGCAAAAAG	5182
Qy	4861	GGAGAAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAAG	4920
Db	5183	GGAGAAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAAG	5242
Qy	4921	CACGAGCTCAGAGTGGCTCTGATGACCACATCAGTGGATGTCCCTGTGTCCCATCTGT	4980
Db	5243	CACGAGCTCAGAGTGGCTCTGATGACCACATCAGTGGATGTCCCTGTGTGTCCCATCTGT	5302
Qy	4981	GTCACTTTTGCATGTCTTCGCCAGCCAGCTTTGCTGATTCTCCGTATCCCAAGAGCGG	5040
Db	5303	GTCACTTTTGCATGTCTTCGCCAGCCAGCTTTGCTGATTCTCCGTATCCCAAGAGCGG	5362
Qy	5041	GTCCAGAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCTGTCACTACTGGCTC	5100
Db	5363	GTCCAGAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCTGTCACTACTGGCTC	5422
Qy	5101	TCTAATTTTGTCTGGGATATGTGCATTAAGTTGTCCCTGCCACACTGGTCAATTATCATC	5160
Db	5423	TCTAATTTTGTCTGGGATATGTGCATTAAGTTGTCCCTGCCACACTGGTCAATTATCATC	5482
Qy	5161	TTCACTCTGCTCCAGCAGAAGTCCATGTGTTGCTCCCAACATCTGCCGTGTACGCCCTT	5220
Db	5483	TTCACTCTGCTCCAGCAGAAGTCCATGTGTTGCTCCCAACATCTGCCGTGTACGCCCTT	5542
Qy	5221	CTACTTTTGTGTATGGTGGTCAATCAACACTCTCATGTACCCAGCCTCCTTTGTGTTTC	5280
Db	5543	CTACTTTTGTGTATGGTGGTCAATCAACACTCTCATGTACCCAGCCTCCTTTGTGTTTC	5602
Qy	5281	AAGATCCCCAGCACACCTATGTGTGTCTACCCAGCTGAACCTCTTCATTGGCATTAAT	5340
Db	5603	AAGATCCCCAGCACACCTATGTGTGTCTACCCAGCTGAACCTCTTCATTGGCATTAAT	5662
Qy	5341	GGCAGCTGGCCACCTTTGCTGGAGCTGTTCAACGGACAATAAGCTGAATAATATCAAT	5400
Db	5663	GGCAGCTGGCCACCTTTGCTGGAGCTGTTCAACGGACAATAAGCTGAATAATATCAAT	5722
Qy	5401	GATATCTGAAGTCCGTTGTTCTTGATCTTCCACATTTTTCCTGGGACAGGCGCTCATC	5460
Db	5723	GATATCTGAAGTCCGTTGTTCTTGATCTTCCACATTTTTCCTGGGACAGGCGCTCATC	5782
Qy	5461	GACATGTTGAAAAACCAAGCAATGGCTGATGCCCTGGAAAAAGTTTGGGGAGAAATCGCTTT	5520
Db	5783	GACATGTTGAAAAACCAAGCAATGGCTGATGCCCTGGAAAAAGTTTGGGGAGAAATCGCTTT	5842
Qy	5521	GTGTCACCATATCTCTGGGACTTGGTGGACAGAAACCTCTTCGCCATGGCCGTGGAAAGG	5580
Db	5843	GTGTCACCATATCTCTGGGACTTGGTGGACAGAAACCTCTTCGCCATGGCCGTGGAAAGG	5902
Qy	5581	GTGTGTTCTTCCTCATTAATCTGTCTGTATCCAGTACAGATTTCTTCATCAGGCCACGACT	5640

Db 5903 GTGGTGTCTCTCATTACTTCTTGATCCAGATACAGATCTCTTATCAGGCCAGACCT 5962
QY 5641 GTAAATGCAAGCTATCTCTCTGAATGATGAAGATGAAGATGTGAGCGGGAAGACAG 5700
Db 5963 GTAAATGCAAGCTATCTCTCTGAATGATGAAGATGAAGATGTGAGCGGGAAGACAG 6022
QY 5701 AGAATCTTGTGATGGTGGAGCCAGATGACATCTTGAATCAAGGAGTTGACGAAGATA 5760
Db 6023 AGAATCTTGTGATGGTGGAGCCAGATGACATCTTGAATCAAGGAGTTGACGAAGATA 6082
QY 5761 TATAGAAGCAAGCGGAGCTGCTGTGACAGGATTTGGTGGGCAATCTCTCTGTGTGAG 5820
Db 6083 TATAGAAGCAAGCGGAGCTGCTGTGACAGGATTTGGTGGGCAATCTCTCTGTGTGAG 6142
QY 5821 TGGTTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCAACTTCAAGATGTTAAACA 5880
Db 6143 TGGTTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCAACTTCAAGATGTTAAACA 6202
QY 5881 GGAGATACCACTGTACAGAGAGATCTTCTTAAACAAAATAGTATCTATCAAAAC 5940
Db 6203 GGAGATACCACTGTACAGAGAGATCTTCTTAAACAAAATAGTATCTATCAAAAC 6262
QY 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGCATGCCATCACAGAGCTG 6000
Db 6263 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGCATGCCATCACAGAGCTG 6322
QY 6001 TTGACTGGGAGAGAACACGTGGAGTTCTTGGCTTTTGAGAGGAGTCCAGAGAAAGAA 6060
Db 6323 TTGACTGGGAGAGAACACGTGGAGTTCTTGGCTTTTGAGAGGAGTCCAGAGAAAGAA 6382
QY 6061 GTTGGCAAGTGTGGTGGGCGGATTCGGAACATGGGCTCGTGAAGTATGGAGAAAAA 6120
Db 6383 GTTGGCAAGTGTGGTGGGCGGATTCGGAACATGGGCTCGTGAAGTATGGAGAAAAA 6442
QY 6121 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db 6443 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6502
QY 6181 GCGGGCCCTCTCTGTGGTGTCTTGGATGAACCCACACAGGATGATCCCAAGCCCGG 6240
Db 6503 GCGGGCCCTCTCTGTGGTGTCTTGGATGAACCCACACAGGATGATCCCAAGCCCGG 6562
QY 6241 CGGTTCTTGTGAATGTGCCCTAGTGTGTCAAGAGGGGAGATCAGTAGTGTATACA 6300
Db 6563 CGGTTCTTGTGAATGTGCCCTAGTGTGTCAAGAGGGGAGATCAGTAGTGTATACA 6622
QY 6301 TCTCATAGTATGAAGAATGTCAAGCTCTTGCACATAGATGGCAATCATGGTCAATGGA 6360
Db 6623 TCTCATAGTATGAAGAATGTCAAGCTCTTGCACATAGATGGCAATCATGGTCAATGGA 6682
QY 6361 AGGTTCAAGTGTCCCTGGCAGTCTCCAGCATCTTAAATAATAGTTTGGAGATGGTTATACA 6420
Db 6683 AGGTTCAAGTGTCCCTGGCAGTCTCCAGCATCTTAAATAATAGTTTGGAGATGGTTATACA 6742
QY 6421 ATAGTGTACGAATAGCAGGGTCCAAACCGGACCTGAGAGCTGCCAGATTTCTTTGGA 6480
Db 6743 ATAGTGTACGAATAGCAGGGTCCAAACCGGACCTGAGAGCTGCCAGATTTCTTTTGA 6802
QY 6481 CTTGCAATTTCTTGGAGTGTCTTAAAGAGAAACACCGGAACATGCTACAATACAGCTT 6540
Db 6803 CTTGCAATTTCTTGGAGTGTCTTAAAGAGAAACACCGGAACATGCTACAATACAGCTT 6862
QY 6541 CCATCTTCATTAATCTTCTGTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAGGGA 6600
Db 6863 CCATCTTCATTAATCTTCTGTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAGGGA 6922
QY 6601 CTCCACATAGAGACTACTCTGTTTCTCAGACACACATTTGACCAAGTATTTGTGAATTT 6660
Db 6923 CTCCACATAGAGACTACTCTGTTTCTCAGACACACATTTGACCAAGTATTTGTGAATTT 6982
QY 6661 GCCAAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 6720
Db 6983 GCCAAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 7042

QY 6721 GTAGTGGAGCTTGACAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAGCTAT 6780
Db 7043 GTAGTGGAGCTTGACAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAGCTAT 7102
QY 6781 GTAT 6784
Db 7103 GTAT 7106

RESULT 4

AAF24686
ID AAF24686 standard; DNA; 10474 BP.

XX AAF24686;
XX AC

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;
XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
XX chromosome 9q22-q31; heart disease; hypercholesterolemia;
XX atherosclerosis; cholesterol transport; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 323..7108

XX FT /*tag= a
XX FT /product= "defective ABC1 polypeptide"

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVTH-) CV THERAPEUTICS INC.

XX Lawn RM, Wade D, Garvin M;

XX WPI; 2001-137812/14.

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
XX useful for the development of agents for the treatment of heart disease
XX and other disorders associated with hypercholesterolemia and
XX atherosclerosis -

XX Disclosure; Page 170-176; 215pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)
XX binding cassette protein (ABC) 1 polypeptide, and is isolated from
XX a Tangier disease patient. ABC1 resides in cell membranes and utilises
XX ATP hydrolysis to transport a wide variety of substrates across the
XX plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
XX mobilisation of intracellular cholesterol stores. ABC1 is defective in
XX Tangier disease, a genetic disorder characterised by abnormal
XX HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
XX 9q22-q31. The ABC1 genes and proteins are useful for developing
XX pharmaceutical agents for the treatment of heart disease and other
XX disorders associated with hypercholesterolemia and atherosclerosis. The
XX genes are useful for developing screening assays to screen for compounds
XX that regulate the expression of genes associated with cholesterol
XX transport. The genes and proteins are also useful for also useful
XX as diagnostic indicators of cardiovascular disease and other disorders
XX associated with hypercholesterolemia.

XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match	100.0%	Score	6782.4	DB	22	Length	10474
Best Local Similarity	100.0%	Pred. No.	0				
Matches	6783	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
Qy	1	ATGGCTTTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAAGAACTTCACTTTTCAGAAAGAAGA	60				
Db	323	ATGGCTTTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAAGAACTTCACTTTTCAGAAAGAAGA	382				
Qy	61	CAACATGTCAGCTGTTACTGGAAGTGGCCTTGCCCTCTATTATCTTCTGATCTCTGATC	120				
Db	383	CAACATGTCAGCTGTTACTGGAAGTGGCCTTGCCCTCTATTATCTTCTGATCTCTGATC	442				
Qy	121	TCTGTGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	180				
Db	443	TCTGTGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC	502				
Qy	181	ATGCCCTCTCAGGAACACTTCCCTTGGCTTCAGGGGATATCTGTAATGCCAACAAACCC	240				
Db	503	ATGCCCTCTCAGGAACACTTCCCTTGGCTTCAGGGGATATCTGTAATGCCAACAAACCC	562				
Qy	241	TGTTTCCGTTACCCGACTCCTGGGAGGCTCCCGAGTGTGTGGAACTTTAACAAATCC	300				
Db	563	TGTTTCCGTTACCCGACTCCTGGGAGGCTCCCGAGTGTGTGGAACTTTAACAAATCC	622				
Qy	301	ATTGTGGCTCGCCTGCTTCAGATGCTCGGAGGCTTCTTTATACAGCAGCAGAAAGACAC	360				
Db	623	ATTGTGGCTCGCCTGCTTCAGATGCTCGGAGGCTTCTTTATACAGCAGCAGAAAGACAC	682				
Qy	361	AGCATGAAGGACATGCGCAAGTCTGAGAACATTCACAGCAGATCAAGAAATCCAGCTCA	420				
Db	683	AGCATGAAGGACATGCGCAAGTCTGAGAACATTCACAGCAGATCAAGAAATCCAGCTCA	742				
Qy	421	AACTTGAAGCTTCAAGATTTCCTGCTGACATGAACCTTCTCTGGGTTCTCTATATCAC	480				
Db	743	AACTTGAAGCTTCAAGATTTCCTGCTGACATGAACCTTCTCTGGGTTCTCTATATCAC	802				
Qy	481	AACCTCTCTCCTCCAAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCTATCTCCAC	540				
Db	803	AACCTCTCTCCTCCAAAGTCTACTGTGACAGATGCTGAGGGCTGATGTCTATCTCCAC	862				
Qy	541	AAGGTATTTTGGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	600				
Db	863	AAGGTATTTTGGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	922				
Qy	601	GAAGAGATGATTCAACTTTGGTGACCAAGAGTTCTGAGCTTTGTGGCTACCAAAGGAG	660				
Db	923	GAAGAGATGATTCAACTTTGGTGACCAAGAGTTCTGAGCTTTGTGGCTACCAAAGGAG	982				
Qy	661	AAACTGGCTGCAGCAGCGAGTACTTCTGTCACATGGACATCCTGAAAGCAATCCCTG	720				
Db	983	AAACTGGCTGCAGCAGCGAGTACTTCTGTCACATGGACATCCTGAAAGCAATCCCTG	1042				
Qy	721	AGAACCTAAACTCTACATCTCCCTTCCGAGCAGGAGCTGGCTGAAGCCACAAAACA	780				
Db	1043	AGAACCTAAACTCTACATCTCCCTTCCGAGCAGGAGCTGGCTGAAGCCACAAAACA	1102				
Qy	781	TGCTGTCATAGCTTTGGGACTCTGCCCAGGAGCTTTCAGCATGAGAAGCTGGAGTGAC	840				
Db	1103	TGCTGTCATAGCTTTGGGACTCTGCCCAGGAGCTTTCAGCATGAGAAGCTGGAGTGAC	1162				
Qy	841	ATGCGACAGGAGGTGATGTTTCTGACCATATGTGAACGCTCAGGTCCTCCACCCCAATC	900				
Db	1163	ATGCGACAGGAGGTGATGTTTCTGACCATATGTGAACGCTCAGGTCCTCCACCCCAATC	1222				
Qy	901	TACCAGGCTGCTCTCGTATTCCTGCGGCAATCCGAGGAGGGGCTTGAGATCAAG	960				
Db	1223	TACCAGGCTGCTCTCGTATTCCTGCGGCAATCCGAGGAGGGGCTTGAGATCAAG	1282				
Qy	961	TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020				
Db	1283	TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1342				

Qy	1021	GAGATGCTGAAACCTCTTATGACAACTCTTACA	CTCTTACTGCAATGATTTGATGAAG	1080
Db	1343	GAGATGCTGAAACCTCTTATGACAACTCTTACA	CTCTTACTGCAATGATTTGATGAAG	1402
Qy	1081	AAATTGGAGTCTAGTCCCTCTTTCCGCAATTA	CTCTTCTGGAAGCTCTGGAAGCCGCTGCTGTT	1140
Db	1403	AAATTGGAGTCTAGTCCCTCTTTCCGCAATTA	CTCTTCTGGAAGCTCTGGAAGCCGCTGCTGTT	1462
Qy	1141	GGGAAGATCCTGTATACACCTGACACTCCAGC	CAACGCAAGGCAGGTCATGGCTGAGGTGAAC	1200
Db	1463	GGGAAGATCCTGTATACACCTGACACTCCAGC	CAACGCAAGGCAGGTCATGGCTGAGGTGAAC	1522
Qy	1201	AAGACCTTCACGAACCTGCTGTGTCCATGATC	TGGAAGCAGTCTGGAGGAAGTCTGAGGAACTCAGC	1260
Db	1523	AAGACCTTCACGAACCTGCTGTGTCCATGATC	TGGAAGCAGTCTGGAGGAAGTCTGAGGAACTCAGC	1582
Qy	1261	CCCAAGATCTGSACTTTCATGTGAGAACACGC	CAAGAAATGACCTTGTCCGATGCTGCTGTTG	1320
Db	1583	CCCAAGATCTGSACTTTCATGTGAGAACACGC	CAAGAAATGACCTTGTCCGATGCTGCTGTTG	1642
Qy	1321	GACAGCAGGACAAATGACACCTTTTGGGACAG	CAGTGGATGCTTAGATTTGACAGAC	1380
Db	1643	GACAGCAGGACAAATGACACCTTTTGGGACAG	CAGTGGATGCTTAGATTTGACAGAC	1702
Qy	1381	CAAGACATCTGGCGTTTTTGGCCAAAGCACC	AGAGGATGCTCCAGTCCAGTAATGGTTCCT	1440
Db	1703	CAAGACATCTGGCGTTTTTGGCCAAAGCACC	AGAGGATGCTCCAGTCCAGTAATGGTTCCT	1762
Qy	1441	GTGTACACCTGGAGAGAACTTTTCAACGAGAC	TACACAGGCAATCCCGAGACCATATCTCGC	1500
Db	1763	GTGTACACCTGGAGAGAACTTTTCAACGAGAC	TACACAGGCAATCCCGAGACCATATCTCGC	1822
Qy	1501	TTCATGAGTGTGTCAACCTGAAACAGCTAGA	ACCCATAGCAACAGAAAGTCTGCTCATC	1560
Db	1823	TTCATGAGTGTGTCAACCTGAAACAGCTAGA	ACCCATAGCAACAGAAAGTCTGCTCATC	1882
Qy	1561	AACAAGTCCATGAGAGTGTGTGATGAGAGAA	GTCTTGGGTGATTTGTTTCACTGGA	1620
Db	1883	AACAAGTCCATGAGAGTGTGTGATGAGAGAA	GTCTTGGGTGATTTGTTTCACTGGA	1942
Qy	1621	ATTACTCCAGCAGCATGAGCTGCCCATCATG	TCACAGTACAAGATCCGAATGGACATT	1680
Db	1943	ATTACTCCAGCAGCATGAGCTGCCCATCATG	TCACAGTACAAGATCCGAATGGACATT	2002
Qy	1681	GACAAATGGAGAGGACAAATAAAATCAAGG	ATGGSTACTGGGACCTTGCTCCGAGCT	1740
Db	2003	GACAAATGGAGAGGACAAATAAAATCAAGG	ATGGSTACTGGGACCTTGCTCCGAGCT	2062
Qy	1741	GACCCCTTTGAGGACATCGGTACGTTCTGGG	GGGCTTCGCTTACTTTCAGAGATGGTG	1800
Db	2063	GACCCCTTTGAGGACATCGGTACGTTCTGGG	GGGCTTCGCTTACTTTCAGAGATGGTG	2122
Qy	1801	GAGCAGGCAATCATCAGGTTGCTGACGGGCA	CCGACGAGAAACCTGCTCTATATGCAA	1860
Db	2123	GAGCAGGCAATCATCAGGTTGCTGACGGGCA	CCGACGAGAAACCTGCTCTATATGCAA	2182
Qy	1861	CAGATGCCCTATCCCTGTTACGTTGATGAC	ATCTTTCGCGGTGATGAGCGGTCAATG	1920
Db	2183	CAGATGCCCTATCCCTGTTACGTTGATGAC	ATCTTTCGCGGTGATGAGCGGTCAATG	2242
Qy	1921	CCCTCTTCTATGACGCTGGCTGGATTTTACT	CAGTGGCTGTGATCATCAAGGGCATCGT	1980
Db	2243	CCCTCTTCTATGACGCTGGCTGGATTTTACT	CAGTGGCTGTGATCATCAAGGGCATCGT	2302
Qy	1981	TATGAGAAGGAGCAGCGCTGAAAGAGACCAT	TCGGATCATGGGCTTGACAAACAGCATA	2040
Db	2303	TATGAGAAGGAGCAGCGCTGAAAGAGACCAT	TCGGATCATGGGCTTGACAAACAGCATA	2362
Qy	2041	CTCTGGTTTACGTTGGTTTCATAGTAGCCCT	ATTCCTTCTTCTGAGCGCTGGCTGCTA	2100
Db	2363	CTCTGGTTTACGTTGGTTTCATAGTAGCCCT	ATTCCTTCTTCTGAGCGCTGGCTGCTA	2422
Qy	2101	GTGCTCATCTGAAATTAGAAACCTGCTGCCCT	ACAGTGAATCCCAAGGCTGGTGTTCCT	2160

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Db 2423 GTGGTCATCTGAAGTTAGGAACCTGCTGGCCCTACAGTGATCCCGAGCGTGGTTTGTG 2482
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QY 2161 TTCTGTGCCGTGTTGCTGTGGTGACAACTCCCTGACGTGCTTCTGATTAGCACACTCTTC 2220
|||||
Db 2483 TTCTGTCCGTGTTGCTGTGGTGACAACTCCCTGACGTGCTTCTGATTAGCACACTCTTC 2542
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QY 2221 TCAGAGCCAACTGGCAGAGCCTGTGGGGGATCATCTACTTCACGTGTACCTGCCC 2280
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Db 2543 TCAGAGCCAACTGGCAGAGCCTGTGGGGGATCATCTACTTCACGTGTACCTGCCC 2602
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QY 2281 TAGCTCTGTGTGGCATGGCAGGACTAGTGGGGTTCACACTCAAGATCTTCGCTAGC 2340
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Db 2603 TAGCTCTGTGTGGCATGGCAGGACTAGTGGGGTTCACACTCAAGATCTTCGCTAGC 2662
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QY 2341 CTGCTGTCTCTGTGCTTTGGGTTTGGCTGTGAGTACTTTGGCCCTTTTGGAGGAGCAG 2400
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Db 2663 CTGCTGTCTCTGTGCTTTGGGTTTGGCTGTGAGTACTTTGGCCCTTTTGGAGGAGCAG 2722
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QY 2401 GGCAATGGAGTGCAGTGGCAGACACCTGTTTGGAGTCCCTGTGGAGGAGATGGCTTCAAT 2460
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Db 2723 GGCAATGGAGTGCAGTGGCAGACACCTGTTTGGAGTCCCTGTGGAGGAGATGGCTTCAAT 2782
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QY 2521 TACATTTGAGCTGCTTTCCAGCCAGTACGGAAATTCAGAGCCTTGGTATTTTCCCTTGC 2580
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QY 2581 ACCAAGTCTACTGTTTGGCAGGAAAGTGTGAGAGCAGCACCTGGTTTCCCAACAG 2640
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Db 2903 ACCAAGTCTACTGTTTGGCAGGAAAGTGTGAGAGCAGCACCTGGTTTCCCAACAG 2962
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Db 2963 AAGAGAAATGTGAGAAATCTGATGAGGAGGAAACCCACCTTGAAGTGGGGGTGCTCC 3022
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Db 3023 ATTGAGAACTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCTGGCA 3082
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QY 2821 ACCACATGTCATCTGACCGGGTGTTCGCCCGACCTCGGCCACCGCTACATCCCTG 2880
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Db 3143 ACCACATGTCATCTGACCGGGTGTTCGCCCGACCTCGGCCACCGCTACATCCCTG 3202
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QY 2881 GGAAGAGACATTGGCTGTGATGATGACACCACTCCGGCAGAAACCTGGGGGTCTGTCCCCAG 2940
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QY 3001 AAAGGCTCTCTGAGAAGCACATGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
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QY 3181 GCTGTGTGGACCTTACTCCCGAGGGGATATGGAGCTGCTGCTGAATATCCGACAA 3240
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Db 3503 GCTGTGTGGACCCCTTACTCCCGCAGGGGAAATATGGGAGCTGCTGCTGAATATCCGACAA 3562
QY 3241 GGCCGACCAATATTCTCTACACACCACTGATGAAGCGGACGCTCTTGGGGGACAGG 3300
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Db 3563 GGCCGACCAATATTCTCTCTACACCACTGATGAAGCGGACGCTCTTGGGGGACAGG 3622
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QY 3301 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGGGCTCTCCCTGTTTCTGAAGAAC 3360
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Db 3623 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGGGCTCTCCCTGTTTCTGAAGAAC 3682
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Db 3683 CAGCTGGGAACAGAGCTACTACTTGACCTTGTCTAAGAAAGATGGAAATCTCCCTCAGT 3742
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QY 3421 TCCTGCAGAAACAGTAGTAGCAGCTGTGTCTATACCTGAAAAGAGGAGGACAGTGTTCCTCAG 3480
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Db 3743 TCCTGCAGAAACAGTAGTAGCAGCTGTGTCTATACCTGAAAAGAGGAGGACAGTGTTCCTCAG 3802
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QY 3481 AGCAGTCTGTATGCTGGCCTGGGAGCAGCAGCATGAGAGTGACACGCTGACCATGCGATGTC 3540
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Db 3863 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAGACATA 3922
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QY 3601 GGGCATGAGCTGACCTATGCTGCCATATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA 3660
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Db 3923 GGGCATGAGCTGACCTATGCTGCCATATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA 3982
|||||
QY 3661 CTCCTTTCATGATGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGCACTCA 3720
|||||
Db 3983 CTCCTTTCATGATGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGCACTCA 4042
|||||
QY 3721 GAGAGACCTTGGAAAGAAATATCTCAAGTGGCCGGAAGAGAGTGGGGTGGATGCTGAG 3780
|||||
Db 4043 GAGAGACCTTGGAAAGAAATATCTCAAGTGGCCGGAAGAGAGTGGGGTGGATGCTGAG 4102
|||||
QY 3781 ACCTCAGATGTTACTCTCCAGCAAGACGAAACAGCGGGGCTTCGGGGGACACAGCAGC 3840
|||||
Db 4103 ACCTCAGATGTTACTCTCCAGCAAGACGAAACAGCGGGGCTTCGGGGGACACAGCAGC 4162
|||||
QY 3841 TGTCTTCCCGGTTTACTGAAAGATGATGCTGCTGATCCAAATGATTTGACATAGACCCA 3900
|||||
Db 4163 TGTCTTCCCGGTTTACTGAAAGATGATGCTGCTGATCCAAATGATTTGACATAGACCCA 4222
|||||
QY 3901 GAATCCAGAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCTTACACAGGTGAA 3960
|||||
Db 4223 GAATCCAGAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCTTACACAGGTGAA 4282
|||||
QY 3961 GGCTGGAACCTTACACAGCAACACTTTTGTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4020
|||||
Db 4283 GGCTGGAACCTTACACAGCAACACTTTTGTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4342
|||||
QY 4021 AGCGGAGTGGAAAGATTTTGTCTCAGTGTCTTGTCCAGCTGTGTTGTCTGCAAT 4080
|||||
Db 4343 AGCGGAGTGGAAAGATTTTGTCTCAGTGTCTTGTCCAGCTGTGTTGTCTGCAAT 4402
|||||
QY 4081 GCCCTTGTGTGACCTGATGCTGCCACCTTTTGGCAAGTACCCCAAGCTTGGAACTTCAG 4140
|||||
Db 4403 GCCCTTGTGTGACCTGATGCTGCCACCTTTTGGCAAGTACCCCAAGCTTGGAACTTCAG 4462
|||||
QY 4141 CCCTGGATGTACAAAGCAAGTACACATTTGTGAGCAATGATGCTCTGAGGACAGGGA 4200
|||||
Db 4463 CCCTGGATGTACAAAGCAAGTACACATTTGTGAGCAATGATGCTCTGAGGACAGGGA 4522
|||||
QY 4201 ACCCTGGAACCTTAAAGCCCTCAGCAAGACCTTGGCTTCGGGACCCGCTGTATGGAA 4260
|||||
Db 4523 ACCCTGGAACCTTAAAGCCCTCAGCAAGACCTTGGCTTCGGGACCCGCTGTATGGAA 4582
|||||
QY 4261 GGAACCCATCCAGACAGCCCTTGCAGGAGGGGAGGAAGTGGACCTGACCTGCCCA 4320
|||||
Db 4583 GGAACCCATCCAGACAGCCCTTGCAGGAGGGGAGGAAGTGGACCTGACCTGCCCA 4642

QY	4321	GTTCCCCAGACCATCATGGAACCTCTTCCAGAATGGGAACCTGGAAATGCGAAGAACCCCTTC	4380
Db	4643	GTTCCCCAGACCATCATGGAACCTCTTCCAGAATGGGAACCTGGCAATGCGAAGAACCCCTTC	4702
QY	4381	CCTGCATGCCAGTAGCAGCGACAAAATCAAGAGATGCTGCCTGTGTCTCCCCCAGG	4440
Db	4703	CCTGCATGCCAGTAGCAGCGACAAAATCAAGAGATGCTGCCTGTGTCTCCCCCAGG	4762
QY	4441	GCAGGGGGTGCTCCTCTCCACAAAGAAAAACAACACTCGAGATATCCTTTCAGSACCTG	4500
Db	4763	GCAGGGGGTGCTCCTCTCCACAAAGAAAAACAACACTCGAGATATCCTTTCAGSACCTG	4822
QY	4501	ACAGGAGAAACATTTCGATTATCTCGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4560
Db	4823	ACAGGAGAAACATTTCGATTATCTCGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4882
QY	4561	TTAAGAACAAGACTCTGGTGAAATGAGTTTAGTTAGTATGGCGCTTTTCCCCTGGGTGCAGT	4620
Db	4883	TTAAGAACAAGACTCTGGTGAAATGAGTTTAGTTAGTATGGCGCTTTTCCCCTGGGTGCAGT	4942
QY	4621	AATACTCACGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAACAACAAATGAAGAA	4680
Db	4943	AATACTCACGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAACAACAAATGAAGAA	5002
QY	4681	CACCTAAAGCTGGCCAAAGCACAGTTCTCGCATGCGATTCTCAACAGCTTGGGAAGATT	4740
Db	5003	CACCTAAAGCTGGCCAAAGCACAGTTCTCGCATGCGATTCTCAACAGCTTGGGAAGATT	5062
QY	4741	ATGACAGGACTGGACACCAAGAAATATGTCAAGGTGTGGTTCAATAACAAGGCTGGCAT	4800
Db	5063	ATGACAGGACTGGACACCAAGAAATATGTCAAGGTGTGGTTCAATAACAAGGCTGGCAT	5122
QY	4801	GCAATCAGCTCTTTTCCCTGAAATGTCATCAACAATGCCATTCTCCGGGGCAAACCTGCAAAAG	4860
Db	5123	GCAATCAGCTCTTTTCCCTGAAATGTCATCAACAATGCCATTCTCCGGGGCAAACCTGCAAAAG	5182
QY	4861	GGAGAGAACCTGACCAATTATGGAATTACTGCTTTCATCATCCCCCTGAATCTCACCAAG	4920
Db	5183	GGAGAGAACCTGACCAATTATGGAATTACTGCTTTCATCATCCCCCTGAATCTCACCAAG	5242
QY	4921	CAGCAGCTCTCAGAGGTGGCTCTGATGACACATCAGTGGATGCTCTGTGTCCATCTGT	4980
Db	5243	CAGCAGCTCTCAGAGGTGGCTCTGATGACACATCAGTGGATGCTCTGTGTCCATCTGT	5302
QY	4981	GTCATCTTTGCAATGTCCTTCTGTCGCCAGCCAGCTTTGTGCTATTCTCTGATCCAGGCGG	5040
Db	5303	GTCATCTTTGCAATGTCCTTCTGTCGCCAGCCAGCTTTGTGCTATTCTCTGATCCAGGCGG	5362
QY	5041	GTCAGCAAGCAAAACACCTGCAAGTTTCATCAGTGGAGTGAAGCCCTGTCATCTACTGGCTC	5100
Db	5363	GTCAGCAAGCAAAACACCTGCAAGTTTCATCAGTGGAGTGAAGCCCTGTCATCTACTGGCTC	5422
QY	5101	TCPTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGCTCATTTATCATC	5160
Db	5423	TCPTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGCTCATTTATCATC	5482
QY	5161	TTCATCTGCTTCCAGCAGAAGTCCATGTGTGCTCCACCAATCTGCTGTGTGTAAGCCCTT	5220
Db	5483	TTCATCTGCTTCCAGCAGAAGTCCATGTGTGCTCCACCAATCTGCTGTGTGTAAGCCCTT	5542
QY	5221	CTACTTTTGTGTATGGGTGGTCAATPCACACCTCTCATGTACCCAGCCTCTCTTTGTGTTTC	5280
Db	5543	CTACTTTTGTGTATGGGTGGTCAATPCACACCTCTCATGTACCCAGCCTCTCTTTGTGTTTC	5602
QY	5281	AAGATCCCCAGCAGACGCTATGTGGTGTCTCACACGCTGAACGCTTCTCATTTGGCATTAAT	5340
Db	5603	AAGATCCCCAGCAGACGCTATGTGGTGTCTCACACGCTGAACGCTTCTCATTTGGCATTAAT	5662
QY	5341	GGCAGCTGGCCACCTTTGTGTGGAGCTGTTTCCACCGACAATAAGCTGAATAATATCAAT	5400
Db	5663	GGCAGCTGGCCACCTTTGTGTGGAGCTGTTTCCACCGACAATAAGCTGAATAATATCAAT	5722

QY	5401	GATATCTCTGAAGTCGGTGTCTTTGATCTTCCACATATTTTGCTCGGACGAGGCTCATC	5460
DB	5723	GATATCTCTGAAGTCGGTGTCTTTGATCTTCCACATATTTTGCTCGGACGAGGCTCATC	5782
QY	5461	GACATGGTGA AAAACACGACCAATGCGTATGCGCTTGGAAAGTTTGGGGAGAAATCGCTTT	5520
DB	5783	GACATGGTGA AAAACACGACCAATGCGTATGCGCTTGGAAAGTTTGGGGAGAAATCGCTTT	5842
QY	5521	GTGTCCACCAATATCTTTGGGACTTTGGTGGGACGAAACCTCTTCCGCAATGCCCTGGAAGGG	5580
DB	5843	GTGTCCACCAATATCTTTGGGACTTTGGTGGGACGAAACCTCTTCCGCAATGCCCTGGAAGGG	5902
QY	5581	GTGGTGTTCTTCTCATTA TACTGTTCTGTATCCAGTACAGATTCTTCATCATGAGCCCGACGCT	5640
DB	5903	GTGGTGTTCTTCTCATTA TACTGTTCTGTATCCAGTACAGATTCTTCATCATGAGCCCGACGCT	5962
QY	5641	GTAAATGCAAACTATCTCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
DB	5963	GTAAATGCAAACTATCTCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	6022
QY	5701	AGAAATCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	5760
DB	6023	AGAAATCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	6082
QY	5761	TATAGAAGGAAGCGGAAGCCTGCTGTTGTACAGATTTGGCTGGCAATCCTCTCTGGTGAG	5820
DB	6083	TATAGAAGGAAGCGGAAGCCTGCTGTTGTACAGATTTGGCTGGCAATCCTCTCTGGTGAG	6142
QY	5821	TGCTTTGGGCTCGCTGGGAGTTAATGGGGCTGGAAATCATCAACTTTCAAGATGTTTAAAC	5880
DB	6143	TGCTTTGGGCTCGCTGGGAGTTAATGGGGCTGGAAATCATCAACTTTCAAGATGTTTAAAC	6202
QY	5881	GGAGATACCACATGTTACCAGAGGAGATGCTTTCCTTTAACAAAAATAGTATCTTATCAAAC	5940
DB	6203	GGAGATACCACATGTTACCAGAGGAGATGCTTTCCTTTAACAAAAATAGTATCTTATCAAAC	6262
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTTACTGCCCTCAGTTTGATGCCATCAGAGCTG	6000
DB	6263	ATCCATGAAGTACATCAGAACATGGGCTTACTGCCCTCAGTTTGATGCCATCAGAGCTG	6322
QY	6001	TTGACTGGGAGAACACAGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCCAGAGAAGAA	6060
DB	6323	TTGACTGGGAGAACACAGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCCAGAGAAGAA	6382
QY	6061	GTTGCAAGGTTGGTGAGTGGGCGATTTCGGAAC TCGGCTCGTGAAGTATGAGAAAAA	6120
DB	6383	GTTGCAAGGTTGGTGAGTGGGCGATTTCGGAAC TCGGCTCGTGAAGTATGAGAAAAA	6442
QY	6121	TATGCTGGTAAC TATAGTGGAGGCAACAACGAACTCTCTACAGCCATGGCTTTGATC	6180
DB	6443	TATGCTGGTAAC TATAGTGGAGGCAACAACGAACTCTCTACAGCCATGGCTTTGATC	6502
QY	6181	GGCGGGCCCTCTGTGGTGTCTTGTGATGAACCCACACAGGCATGGATCCAAAGCCCGG	6240
DB	6503	GGCGGGCCCTCTGTGGTGTCTTGTGATGAACCCACACAGGCATGGATCCAAAGCCCGG	6562
QY	6241	CGGTTCTTGGAATTTGTGCCCTTAAGTGTGTCAAGAGGGGAGATCAGTAGTGCTTACA	6300
DB	6563	CGGTTCTTGGAATTTGTGCCCTTAAGTGTGTCAAGAGGGGAGATCAGTAGTGCTTACA	6622
QY	6301	TCTCATAGTATGAAGAA TGTGAAGCTCTTTGAC TAGGATGGCAATCATGGTCAATGGA	6360
DB	6623	TCTCATAGTATGAAGAA TGTGAAGCTCTTTGAC TAGGATGGCAATCATGGTCAATGGA	6682
QY	6361	AGGTTCAGGTGCCCTTGGCAGTGTCCACGATCTTAAAAAATAGTTTGGAGATGTTTATACA	6420
DB	6683	AGGTTCAGGTGCCCTTGGCAGTGTCCACGATCTTAAAAAATAGTTTGGAGATGTTTATACA	6742
QY	6421	ATAGTTGTACGAATAGCAGGTC CAAACCCGAGCTGAGGCTCTCCAGGATTTCTTTTGA	6480
DB	6743	ATAGTTGTACGAATAGCAGGTC CAAACCCGAGCTGAGGCTCTCCAGGATTTCTTTTGA	6802
QY	6481	CTTGCACTTTCTCTGGAAGTGTCTTAAAAGAGAAACACCGGAACATGCTTACAATACCACTT	6540

Db	6803	CTTGCAATTCCTGGAAAGTGTCTTAAAGAGAACACCGGAACATGCTACATACCAGCTT	6862
Qy	6541	CCATCTTCATTATCTTCTCTGGCCAGGATATTTCAGCATCTCTCTCCAGAGCAAAAAGCGA	6600
Db	6863	CCAATCTTCATTATCTTCTCTGGCCAGGATATTTCAGCATCTCTCTCCAGAGCAAAAAGCGA	6922
Qy	6601	CTCCACATAGAAGACTACTCTGTCTTCTCAGACAACACTTGGACCAAGTATTTGTGAACCTTT	6660
Db	6923	CTCCACATAGAAGACTACTCTGTCTTCTCAGACAACACTTGGACCAAGTATTTGTGAACCTTT	6982
Qy	6661	GCCAAGGACCAAAAGTGATGATGACCACCTTAAAGACCTCTCATTTACACAAAAACCAGACA	6720
Db	6983	GCCAAGGACCAAAAGTGATGATGACCACCTTAAAGACCTCTCATTTACACAAAAACCAGACA	7042
Qy	6721	GTAGTGCACGCTTCACGCTTCTTCACATCTTTTCTTACAGGATGAGAAGTGAAAGAAAGCTAT	6780
Db	7043	GTAGTGCACGCTTCGAGCTTCTTCACATCTTTTCTTACAGGATGAGAAGTGAAAGAAAGCTAT	7102
Qy	6781	GTAT GTAT 6784	
Db	7103	GTAT 7106	
RESULT 5			
AAF24707			
ID AAF24707 standard; DNA; 10474 BP			

RESULT 5	
AAF24707	
ID	AAF24707 standard; DNA; 10474 BP.
XX	
XX	
AC	AAF24707;
XX	
XX	
DT	20-APR-2001 (first entry)
XX	
XX	
DE	Nucleotide sequence of AAF24707 from Tangier disease patient.

XX	WO200078971-A2.
PN	
XX	
XX	28-DEC-2000.
PD	
XX	
XX	16-JUN-2000; 2000WO-US16591.
XX	
XX	18-JUN-1999; 99US-0140264.
PR	14-SEP-1999; 99US-0153872.
PR	19-NOV-1999; 99US-0166573.
XX	
XX	{CVTH-} CV THERAPEUTICS INC.
PA	(UNITW) UNIV WASHINGTON.
PA	
XX	
XX	Lawn RM, Wade D, Oram JF, Garvin M;
PI	
XX	WPI; 2001-137811/14.
DR	P-PSDB; AAB31366.
DR	
XX	
PT	Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT	polynucleotides and polypeptides, useful for treatment of heart disease
PT	and other disorders associated with hypercholesterolemia and
PT	atherosclerosis -
XX	
XX	Claim 27; Page 144-150; 211pp; English.
PS	
XX	
XX	The present sequence encodes a human adenosine triphosphate (ATP)
CC	binding cassette protein (ABC) 1 polypeptide, and is isolated from

QY 781 TTGCTCATAGTCTTGGGACTCTGGCCAGGAGCTGTTACGATGAGAGCTGGAGTAC 840
 DB 1103 TTGCTCATAGTCTTGGGACTCTGGCCAGGAGCTGTTACGATGAGAGCTGGAGTAC 1162
 QY 841 ATGCGACAGAGTGATGTTCTGACCAATGTGACAGCTGACAGCTCTCCACCAATC 900
 DB 1163 ATGCGACAGAGTGATGTTCTGACCAATGTGACAGCTGACAGCTCTCCACCAATC 1222
 QY 901 TACAGGCTGTGTCTCGTATGTTCTGCGGCATCCGAGGAGGGGGCTGAAGATCAAG 960
 DB 1223 TACAGGCTGTGTCTCGTATGTTCTGCGGCATCCGAGGAGGGGGCTGAAGATCAAG 1282
 QY 961 TCTCTCAACTGGTATGAGGACAACTACAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
 DB 1283 TCTCTCAACTGGTATGAGGACAACTACAAGCCCTCTTTGGAGGCAATGGCACTGAG 1342
 QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTGATGAAG 1080
 DB 1343 GAAGATGCTGAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTGATGAAG 1402
 QY 1081 AATTTGGAGTCTAGTCTCTTTCCSCATATCTGGAAGCTCTGAAGCCGCTGCTGTT 1140
 DB 1403 AATTTGGAGTCTAGTCTCTTTCCSCATATCTGGAAGCTCTGAAGCCGCTGCTGTT 1462
 QY 1141 GGAAGATCTGTATACACTGACATCCAGCCACAGCAGTCAATGCTGAGTGAAC 1200
 DB 1463 GGAAGATCTGTATACACTGACATCCAGCCACAGCAGTCAATGCTGAGTGAAC 1522
 QY 1201 AAGACCTTCCAGGAATGGTGTGTTCCATGATCTGGAAGCAATGTTGGAGGAACCTCAGC 1260
 DB 1523 AAGACCTTCCAGGAATGGTGTGTTCCATGATCTGGAAGCAATGTTGGAGGAACCTCAGC 1582
 QY 1261 CCCAAGATCTGACCTTCATGGAGACAGCCAGAAATGGACCTTGTCCGGATGCTGTTG 1320
 DB 1583 CCCAAGATCTGACCTTCATGGAGACAGCCAGAAATGGACCTTGTCCGGATGCTGTTG 1642
 QY 1321 GACAGCAGGACAAATGACCACTTTTGGACACAGCAGTTGATGGCTTAGATTGGACAGCC 1380
 DB 1643 GACAGCAGGACAAATGACCACTTTTGGACACAGCAGTTGATGGCTTAGATTGGACAGCC 1702
 QY 1381 CAGACATCTGGGCTTTTGGCCAGCAGCCAGAGATGTCAGTCCAGTAAATGTTCT 1440
 DB 1703 CAGACATCTGGGCTTTTGGCCAGCAGCCAGAGATGTCAGTCCAGTAAATGTTCT 1762
 QY 1441 GTGTACACCTGGAGAGAGCTTTCAAGGAGCTAACCCAGCAATCCGAGCAATCTCTGC 1500
 DB 1763 GTGTACACCTGGAGAGAGCTTTCAAGGAGCTAACCCAGCAATCCGAGCAATCTCTGC 1822
 QY 1501 TTCTAGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGAACAGAGTCTGGCTCATC 1560
 DB 1823 TTCTAGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGAACAGAGTCTGGCTCATC 1882
 QY 1561 AACAGTCCATGGAGCTGCTGGATGAGAGAGTCTCTGGCTGTTATGTTCACTGGA 1620
 DB 1883 AACAGTCCATGGAGCTGCTGGATGAGAGAGTCTCTGGCTGTTATGTTCACTGGA 1942
 QY 1621 ATTACTCCAGCAGCATTTGAGTCTCCCATCATGTCTCAAGTACAAGATCCGAATGGACATT 1680
 DB 1943 ATTACTCCAGCAGCATTTGAGTCTCCCATCATGTCTCAAGTACAAGATCCGAATGGACATT 2002
 QY 1681 GACAATGTGGAGGACAAATAAATCAAGATGGGTACTGGGACCTGCTCTCGAGCT 1740
 DB 2003 GACAATGTGGAGGACAAATAAATCAAGATGGGTACTGGGACCTGCTCTCGAGCT 2062
 QY 1741 GACCCCTTTGAGGACATGCGTACGCTGGGGGCTTCGCCTACTTGCAGGATGTGGT 1800
 DB 2063 GACCCCTTTGAGGACATGCGGTACGCTGGGGGCTTCGCCTACTTGCAGGATGTGGT 2122
 QY 1801 GAGCAGGCAATCATCAGGGTCTGACGGGACCGAGAGAAACTGGTGTCTATATGCAA 1860
 DB 2123 GAGCAGGCAATCATCAGGGTCTGACGGGACCGAGAGAAACTGGTGTCTATATGCAA 2182
 QY 1861 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTTCTGGGGTGATGACCGGCTCATG 1920

DB 2183 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTTCGCGGGTATGAGCCGGTCAATG 2242
 QY 1921 CCCCTCTTACATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980
 DB 2243 CCCCTCTTACATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 2302
 QY 1981 TATGAGAAGGAGGACCGCTGAAGAGACCATGGGATCATGGGCTGGACAAAGCAATA 2040
 DB 2303 TATGAGAAGGAGGACCGCTGAAGAGACCATGGGATCATGGGCTGGACAAAGCAATA 2362
 QY 2041 CTCTGCTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCTGCTA 2100
 DB 2363 CTCTGCTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCTGCTA 2422
 QY 2101 GTGTCCTCATCTGAAGTTAGGAACCTGCTGGCCTACAGATGATCCAGCGTGGTGTTC 2160
 DB 2423 GTGTCCTCATCTGAAGTTAGGAACCTGCTGGCCTACAGTATCCAGCGTGGTGTTC 2482
 QY 2161 TTCCCTGTCGCTGTTGCTGTGTGAGCAATCTCTGAGTCTTCTCTGATTAGCACACTTTC 2220
 DB 2483 TTCCCTGTCGCTGTTGCTGTGTGAGCAATCTCTGAGTCTTCTCTGATTAGCACACTTTC 2542
 QY 2221 TCCAGAGCCAACTGGCAGACCTGTGGGGCATCATCTACTTACACGCTGTACCTGCC 2280
 DB 2543 TCCAGAGCCAACTGGCAGACCTGTGGGGCATCATCTACTTACACGCTGTACCTGCC 2602
 QY 2281 TACGTCCTGTGTGGCAGTGGCAGACTACGTTGGGCTTCACACTCAAGATCTTCCTAGC 2340
 DB 2603 TACGTCCTGTGTGGCAGTGGCAGACTACGTTGGGCTTCACACTCAAGATCTTCCTAGC 2662
 QY 2341 CTGCTGTCCTGCTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTCAGGAGCAG 2400
 DB 2663 CTGCTGTCCTGCTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTCAGGAGCAG 2722
 QY 2401 GGCATTGGAGTCACTGGGACAACTGTTTGGAGTCTCTGTGGAGAGAGATGCTTCAAT 2460
 DB 2723 GGCATTGGAGTCACTGGGACAACTGTTTGGAGTCTCTGTGGAGAGAGATGCTTCAAT 2782
 QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGTGACCTGG 2520
 DB 2783 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGTGACCTGG 2842
 QY 2521 TACATTGAGGCTGTCTTCCAGCCAGTACGGAATTTCCAGGCCCTGTGATTTCTTCC 2580
 DB 2843 TACATTGAGGCTGTCTTCCAGCCAGTACGGAATTTCCAGGCCCTGTGATTTCTTCC 2902
 QY 2581 ACCAAGTCTCTACTGTTTGGCGAGGAAAGTATGAGAGAGCACCCTGTTTCCAAACAG 2640
 DB 2903 ACCAAGTCTCTACTGTTTGGCGAGGAAAGTATGAGAGAGCACCCTGTTTCCAAACAG 2962
 QY 2641 AAGAGAAATGTCAAAAATCTGCATGGAGGAGAACCCACCCACTTTGAAGCTGGGCGTGTCC 2700
 DB 2963 AAGAGAAATGTCAAAAATCTGCATGGAGGAGAACCCACCCACTTTGAAGCTGGGCGTGTCC 3022
 QY 2701 ATTCAGAACCTTGTAAGTCTACCGAGATGGATGAAAGTGGCTGTCTCGATGGCTGGCA 2760
 DB 3023 ATTCAGAACCTTGTAAGTCTACCGAGATGGATGAAAGTGGCTGTCTCGATGGCTGGCA 3082
 QY 2761 CTGAATTTTATGAGGGCCAGATCAGCTCTCTCTGGGCCACAATGAGCGGGAAGAGC 2820
 DB 3083 CTGAATTTTATGAGGGCCAGATCAGCTCTCTCTGGGCCACAATGAGCGGGAAGAGC 3142
 QY 2821 ACCACCATGTCAATCTCTACCGGGTGTTCCTCCCGGACCTTCGGGACCCGCTTACATCTCG 2880
 DB 3143 ACCACCATGTCAATCTCTACCGGGTGTTCCTCCCGGACCTTCGGGACCCGCTTACATCTCG 3202
 QY 2881 GGAAGACATTCGCTCTGAGATGACCAATCCGCAAGAACTGGGGTCTGTCTCCCGAG 2940
 DB 3203 GGAAGACATTCGCTCTGAGATGACCAATCCGCAAGAACTGGGGTCTGTCTCCCGAG 3262
 QY 2941 CATAAGCTGCTGTTGACATGCTGACTGTGGAAGAACACATCTGTTCTATGCCCGCTTG 3000

Db 3263 CATACGCTGCTGTTGACATGCTGACTGTGTGAAGAACACATCTGTTCTATGCGCGTTG 3322
 QY 3001 AAAGGGCTCTCTGAGAACGACGTGAAGCGGAGATGAGCAGATGCCCTGGATGTTGGT 3060
 Db 3323 AAAGGGCTCTCTGAGAACGACGTGAAGCGGAGATGAGCAGATGCCCTGGATGTTGGT 3382
 QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCAAGTGGATGCAAGAAAG 3120
 Db 3383 TTGCCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCAAGTGGATGCAAGAAAG 3442
 QY 3121 CTATCTGTGGCTTGGCTTTGCTGGGGATCTAAAGTTGTCAATCTGATGAACCCACA 3180
 Db 3443 CTATCTGTGGCTTGGCTTTGCTGGGGATCTAAAGTTGTCAATCTGATGAACCCACA 3502
 QY 3181 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCCACAA 3240
 Db 3503 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCCACAA 3562
 QY 3241 GGCGGACCACTTATCTCTCTACACACACATGGATGAAGCGACGTCTCTGGGGACAGG 3300
 Db 3563 GGCGGACCACTTATCTCTCTACACACACATGGATGAAGCGACGTCTCTGGGGACAGG 3622
 QY 3301 ATTGCCATCATCTCCCATGSGAAGCTGTGCTGTGGGTCTCTCCCTGTTCTGAAGAAC 3360
 Db 3623 ATTGCCATCATCTCCCATGSGAAGCTGTGCTGTGGGTCTCTCCCTGTTCTGAAGAAC 3682
 QY 3361 CAGCTGGGAACAGCTTACTACCTTGGTCAAGAAAGATGTGGAATCTCTCCCTCAGT 3420
 Db 3683 CAGCTGGGAACAGCTTACTACCTTGGTCAAGAAAGATGTGGAATCTCTCCCTCAGT 3742
 QY 3421 TCCTGAGAAACAGTGTAGTGTCTATACCTGAAAGAGGACAGTGTCTCTAG 3480
 Db 3743 TCCTGAGAAACAGTGTAGTGTCTATACCTGAAAGAGGACAGTGTCTCTAG 3802
 QY 3481 AGCAGTCTGTATGCTGGCTGGCAGCAGCATGAGAGTGTACACCTGACCATGATGTC 3540
 Db 3803 AGCAGTCTGTATGCTGGCTGGCAGCAGCATGAGAGTGTACACCTGACCATGATGTC 3862
 QY 3541 TCTGCTATCTCAACCTCTATCAGGAGCATGTCTGAGCCCGCTGGTGAACACATA 3600
 Db 3863 TCTGCTATCTCAACCTCTATCAGGAGCATGTCTGAGCCCGCTGGTGAACACATA 3922
 QY 3601 GGCATGAGCTGACCTATGCTGCTCATATGAAGCTGTAAAGAGGAGCCCTTTGTGAA 3660
 Db 3923 GGCATGAGCTGACCTATGCTGCTCATATGAAGCTGTAAAGAGGAGCCCTTTGTGAA 3982
 QY 3661 CTCTTTATGAGATGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTATGGCATCTCA 3720
 Db 3983 CTCTTTATGAGATGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTATGGCATCTCA 4042
 QY 3721 GAGACGACCTTGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGTGATGCTCAG 3780
 Db 4043 GAGACGACCTTGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGTGATGCTCAG 4102
 QY 3781 ACCTCAGATGATGATGCTGCCAGCAGAAACAGCGCGGCTTGGGGGCAAGCAGAGC 3840
 Db 4103 ACCTCAGATGATGATGCTGCCAGCAGAAACAGCGCGGCTTGGGGGCAAGCAGAGC 4162
 QY 3841 TGTCTTCGCGCTTCACTGAAGATGATGCTGCTATCCAAATGATTTCTGACATAGACCA 3900
 Db 4163 TGTCTTCGCGCTTCACTGAAGATGATGCTGCTATCCAAATGATTTCTGACATAGACCA 4222
 QY 3901 GAATCCAGAGACAGATGCTGCTAGTGGATGGATGGCAAGGGTCTCTACAGGTGAAA 3960
 Db 4223 GAATCCAGAGACAGATGCTGCTAGTGGATGGATGGCAAGGGTCTCTACAGGTGAAA 4282
 QY 3961 GGCTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATGGC 4020
 Db 4283 GGCTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATGGC 4342
 QY 4021 AGACGGATCGGAAGGATTTTTGCTCAGATGCTTGTGCGAGCTGTGTTGCTGCTGAT 4080
 Db 4343 AGACGGATCGGAAGGATTTTTGCTCAGATGCTTGTGCGAGCTGTGTTGCTGCTGAT 4402

QY 4081 GCCTTGTGTTTTCAGCTGTATGCTGACCCCTTTTGCAAGTACCCAGCCTGGAATCTCAG 4140
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 QY 4141 CCCTGATGTACAACGACAGTACATTTGTCAGCAATGATGCTCCTTGAGACACGGGA 4200
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DB 7103 GTAT 7106

RESULT 6
AAF24708
ID AAF24708 standard; DNA; 10474 BP.
XX AAF24708;
AC AAF24708;
XX 20-APR-2001 (first entry)
XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
DE Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 323..7108
FT CDS /*tag= a
FT /product= "defective ABC1 polypeptide"
XX WO200078971-A2.
XX 28-DEC-2000.
PD 16-JUN-2000; 2000WO-US16591.
XX 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX (CVTH-) CV THERAPEUTICS INC.
PA

(UNIW) UNIV WASHINGTON.

Lawn RM, Wade D, Oram JF, Garvin M:

WPI: 2001-137811/14.

WPI; 2001-13/811/
P-PSDB: AAB31367

Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and

atherosclerosis -

Claim 30: Page 16

2000

The present sequence encodes a human ad-

binding cassette protein (ABC1) polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-q9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

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every Match      100.0%; Score 6782.4; DB 22; Length 10474;
t Local Similarity 100.0%; Pred. No. 0;
ches 6783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 3323 AAAGGGCTCTCTGAGAAGCAGTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT 3382
QY 3061 TTGCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCAAGTGAATCCAGAGAAAG 3120
Db 3383 TTGCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCAAGTGAATCCAGAGAAAG 3442
QY 3121 CTATCTGTGGCTTGGCCCTTGTGCGGGATCTAAGGTGTCTATCTGGATGAACCCACA 3180
Db 3443 CTATCTGTGGCTTGGCCCTTGTGCGGGATCTAAGGTGTCTATCTGGATGAACCCACA 3502
QY 3181 GGTGTGTGGACCTTACTCCGAGAGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3240
Db 3503 GCTGTGTGGACCTTACTCCGAGAGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3562
QY 3241 GCGCCACCATTTATCTCTACACACACATGATGAAGCGGAGCTCCTGGGGACAGG 3300
Db 3563 GCGCCACCATTTATCTCTACACACACATGATGAAGCGGAGCTCCTGGGGACAGG 3622
QY 3301 ATTGGCATCTCTCCATGGGAAGCTGTGTGTGGGCTCCTCCTCTTCTGAAAGAC 3360
Db 3623 ATTGGCATCTCTCCATGGGAAGCTGTGTGTGGGCTCCTCCTCTTCTGAAAGAC 3682
QY 3361 CAGCTGGGAACAGGCTACTACTGACCTTGTGTTGCTGAAGAAAGATGTGGAATCCTCCTCAGT 3420
Db 3683 CAGCTGGGAACAGGCTACTACTGACCTTGTGTTGCTGAAGAAAGATGTGGAATCCTCCTCAGT 3742
QY 3421 TCCTCGAAGACAGTAGTAGCCTGTGTACCTGTAACCTGTAAGAAAGAGGACAGTGTCTCAG 3480
Db 3743 TCCTCGAAGACAGTAGTAGCCTGTGTACCTGTAACCTGTAAGAAAGAGGACAGTGTCTCAG 3802
QY 3481 AGCAGTTCGTGCTGGCTGGGACGACCATGAGAGTGAACCTGACACCTGACCATCGATGTC 3540
Db 3803 AGCAGTTCGTGCTGGCTGGGACGACCATGAGAGTGAACCTGACCATCGATGTC 3862
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTGTAAGCCCGGCTGGTGAAGACATA 3600
Db 3863 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTGTAAGCCCGGCTGGTGAAGACATA 3922
QY 3601 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGTCTAAGGAGGAGCTTGTGGAA 3660
Db 3923 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGTCTAAGGAGGAGCTTGTGGAA 3982
QY 3661 CTCCTTTCATGAGATGATGACCGCTCTCAGACCTGGGCAATTCCTAGTATGGCATCTCA 3720
Db 3983 CTCCTTTCATGAGATGATGACCGCTCTCAGACCTGGGCAATTCCTAGTATGGCATCTCA 4042
QY 3721 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAGAGAGTGGGTGATGCTGAG 3780
Db 4043 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAGAGAGTGGGTGATGCTGAG 4102
QY 3781 ACCTCAGATGTACCTTCCAGCAAGCAAGAGCGCGGCTTCGGGGACAAAGCAGAGC 3840
Db 4103 ACCTCAGATGTACCTTCCAGCAAGCAAGAGCGCGGCTTCGGGGACAAAGCAGAGC 4162

QY 3841 TGTCTCGCCCGTTCACATGAAGATGATGCTGCTGATCCAAATGATCTGACATAGACCA 3900
 Db 4163 TGTCTCGCCCGTTCACATGAAGATGATGCTGCTGATCCAAATGATCTGACATAGACCA 4222
 QY 3901 GAATCCAGAGACAGACTTGTCTAGTGGATGGATGGCAAGGGTCTTACAGGTGAAA 3960
 Db 4223 GAATCCAGAGACAGACTTGTCTAGTGGATGGATGGCAAGGGTCTTACAGGTGAAA 4282
 QY 3961 GGTGGAACTTACACAGACAGTGTGCGCCCTTTTGTGGAAGAGACTGCTAATGCC 4020
 Db 4283 GGTGGAACTTACACAGACAGTGTGCGCCCTTTTGTGGAAGAGACTGCTAATGCC 4342
 QY 4021 AGACGAGTCGGAAGAGATTTTGTCTCAGATTTGCTTGCACAGTGTGTTGTCTGCAAT 4080
 Db 4343 AGACGAGTCGGAAGAGATTTTGTCTCAGATTTGCTTGCACAGTGTGTTGTCTGCAAT 4402
 QY 4081 GCGCTGTGTTACAGCTGATGCTGCCACCCCTTGGCAAGTACCCAGCTGGAATTCAG 4140
 Db 4403 GCGCTGTGTTACAGCTGATGCTGCCACCCCTTGGCAAGTACCCAGCTGGAATTCAG 4462
 QY 4141 CCTGGATGTACAAGAACAGTACATTTGTTCAGCAATGATGCTCTGAGGACACGGGA 4200
 Db 4463 CCTGGATGTACAAGAACAGTACATTTGTTCAGCAATGATGCTCTGAGGACACGGGA 4522
 QY 4201 ACCCTGGAACTTTAAAGCCCTTACCAAGACCCCTGCTCGGGACCCGCTGTATGAA 4260
 Db 4523 ACCCTGGAACTTTAAAGCCCTTACCAAGACCCCTGCTCGGGACCCGCTGTATGAA 4582
 QY 4261 GGAACCCAAATCCCAAGACACGCGCTGCCAGGAGGGAGAGAGTGGACCACTGCCCA 4320
 Db 4583 GGAACCCAAATCCCAAGACACGCGCTGCCAGGAGGGAGAGAGTGGACCACTGCCCA 4642
 QY 4321 GTTCCCAAGACCATGGAACCTCTTCAGAAATGGGAATGGCAATGGCAATGGCAACCTTCA 4380
 Db 4643 GTTCCCAAGACCATGGAACCTCTTCAGAAATGGGAATGGCAATGGCAACCTTCA 4702
 QY 4381 CCGTATGCTGCTAGTGTAGGAGGACAAATCAAGAGATGCTGCTGTGTCGCCCGAGG 4440
 Db 4703 CCGTATGCTGCTAGTGTAGGAGGACAAATCAAGAGATGCTGCTGTGTCGCCCGAGG 4762
 QY 4441 GCAGGGGCTGCTCTCCCAAGAAACAAACACTGCAGATATGCTTTCAGGACTG 4500
 Db 4763 GCAGGGGCTGCTCTCCCAAGAAACAAACACTGCAGATATGCTTTCAGGACTG 4822
 QY 4501 ACAGGAAGAAATTCGGATATCTGCTGAGAGAGTATGCTGAGATATGAGCAATGAGCA 4560
 Db 4823 ACAGGAAGAAATTCGGATATCTGCTGAGAGAGTATGCTGAGATATGAGCAATGAGCA 4882
 QY 4561 TTAAAGAAACAGATCTGGTGAATGAGTTTATGATGCGGCTTTTCCCTGGGTGTCAGT 4620
 Db 4883 TTAAAGAAACAGATCTGGTGAATGAGTTTATGATGCGGCTTTTCCCTGGGTGTCAGT 4942
 QY 4621 AATCTCAAGCACTTCTCCAGTCAAGAGTTAATGATGCCATCAACAAATGAGAAA 4680
 Db 4943 AATCTCAAGCACTTCTCCAGTCAAGAGTTAATGATGCCATCAACAAATGAGAAA 5002
 QY 4681 CACCTAAAGCTGGCCAGGACAGTCTGACATGATTTCTCAACAGCTTGGGAAGATT 4740
 Db 5003 CACCTAAAGCTGGCCAGGACAGTCTGACATGATTTCTCAACAGCTTGGGAAGATT 5062
 QY 4741 ATGACAGACTGGACACAGAAATTAATGCAAGTGTGGTTTCAATATACAGGGCTGGCAT 4800
 Db 5063 ATGACAGACTGGACACAGAAATTAATGCAAGTGTGGTTTCAATATACAGGGCTGGCAT 5122
 QY 4801 GCAATCAGCTCTTCTCGTGAATGCTCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 4860
 Db 5123 GCAATCAGCTCTTCTCGTGAATGCTCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 5182
 QY 4861 GGAGAAACCCCTAGCCATTTAGGAATTTACTGCTTTCAATATCCCTGAAATCTCAACCAAG 4920
 Db 5183 GGAGAAACCCCTAGCCATTTAGGAATTTACTGCTTTCAATATCCCTGAAATCTCAACCAAG 5242

QY 4921 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTTGTCATCTGT 4980
 Db 5243 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTTGTCATCTGT 5302
 QY 4981 GTCATCTTTGCAATGCTCTTCTGTCACAGAGCTTTGCTATTTCTGATCTCAGGAGCGG 5040
 Db 5303 GTCATCTTTGCAATGCTCTTCTGTCACAGAGCTTTGCTATTTCTGATCTCAGGAGCGG 5362
 QY 5041 GTCAGCAAAAGCAAAACACTTGCAGTTTCATGAGTGGAGCTGATCTACTGCTC 5100
 Db 5363 GTCAGCAAAAGCAAAACACTTGCAGTTTCATGAGTGGAGTGAAGCTGCTACTACTGCTC 5422
 QY 5101 TCTAATTTTGTCTGGGATATGTCATTTAGTGTCTCCTGCCACACTGGTTCATATATCATC 5160
 Db 5423 TCTAATTTTGTCTGGGATATGTCATTTAGTGTCTCCTGCCACACTGGTTCATATATCATC 5482
 QY 5161 TTCATCTGCTTCCAGCAGAGTCTTATGTCCTCTCCACCAATCTGCTGTCAGGCTT 5220
 Db 5483 TTCATCTGCTTCCAGCAGAGTCTTATGTCCTCTCCACCAATCTGCTGTCAGGCTT 5542
 QY 5221 CTACTTTTGTCTGATGGTGTCAATCAGTGTCTCTCATGTACCCAGCTCTCTTTGTTTC 5280
 Db 5543 CTACTTTTGTCTGATGGTGTCAATCAGTGTCTCTCATGTACCCAGCTCTCTTTGTTTC 5602
 QY 5281 AAGATCCCAAGCAGCTATGTCCTCACCAGGCTGAACCTCTTCATTTGSCATTAAT 5340
 Db 5603 AAGATCCCAAGCAGCTATGTCCTCACCAGGCTGAACCTCTTCATTTGSCATTAAT 5662
 QY 5341 GGCAGCTGCTGCCACCTTTGTGCTGGAGCTTCCACGACAAATGAAGTATATATCAAT 5400
 Db 5663 GGCAGCTGCTGCCACCTTTGTGCTGGAGCTTCCACGACAAATGAAGTATATATCAAT 5722
 QY 5401 GATATCCTGAAGTCCGTTTCTTGTCTTCCACATTTTTCCTGGGAGGAGGCTCATC 5460
 Db 5723 GATATCCTGAAGTCCGTTTCTTGTCTTCCACATTTTTCCTGGGAGGAGGCTCATC 5782
 QY 5461 GACATGTGAAACAGCAATGGCTGATGCTTCCCTGGAAGGTTTGGGAGATGCTCTT 5520
 Db 5783 GACATGTGAAACAGCAATGGCTGATGCTTCCCTGGAAGGTTTGGGAGATGCTCTT 5842
 QY 5521 GTGTACCATTTATCTTGGGACTTGGTGGGACGAAACCTCTTCCCATGCTGCGGAGG 5580
 Db 5843 GTGTACCATTTATCTTGGGACTTGGTGGGACGAAACCTCTTCCCATGCTGCGGAGG 5902
 QY 5581 GTGGTGTCTCTCATTTACTGTTCTGATCCAGTACAGATCTTTCATCAGGCGCCAGCT 5640
 Db 5903 GTGGTGTCTCTCATTTACTGTTCTGATCCAGTACAGATCTTTCATCAGGCGCCAGCT 5962
 QY 5641 GTAAATGCAAGCTATCTCTCTGAATGATGAAGTGAAGATGTAGAGGCGGGAAGACAG 5700
 Db 5963 GTAAATGCAAGCTATCTCTCTGAATGATGAAGTGAAGATGTAGAGGCGGGAAGACAG 6022
 QY 5701 AGAATCTTGATGGTGGAGCCAGATGACATCTTGAAGTCAAGAGTGTAGCAAGATA 5760
 Db 6023 AGAATCTTGATGGTGGAGCCAGATGACATCTTGAAGTCAAGAGTGTAGCAAGATA 6082
 QY 5761 TATAGAAGAAAGCGGAGCTGCTGTTGACAGATTTGCTGGGCAATTCCTCTGTTGAG 5820
 Db 6083 TATAGAAGAAAGCGGAGCTGCTGTTGACAGATTTGCTGGGCAATTCCTCTGTTGAG 6142
 QY 5821 TGTCTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCACTTTCAAGATGTTAACA 5880
 Db 6143 TGTCTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCACTTTCAAGATGTTAACA 6202
 QY 5881 GGAGTACCACTGTTACAGAGAGAGTGTCTTCTTAAACAAATAGTATCTTATCAAC 5940
 Db 6203 GGAGTACCACTGTTACAGAGAGAGTGTCTTCTTAAACAAATAGTATCTTATCAAC 6262
 QY 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
 Db 6263 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6322
 QY 6001 TTGACTGGGAGAACACAGTGGAGTTCTTTGCTCTTTTGAGAGGAGTCCCGAGGAAGAA 6060

Db	6323	TTGACTGGGAGAGAACAGTGGAGTCTTTGCCCTTTTGAGAGAGTCCCCAGAGAAGAA	6382
Qy	6061	GTTCGCAAGTGGTGGTGGCGATTCCGAAACTGGGCCCTCGTGAAGTATGGAGAAAA	6120
Db	6383	GTTCGCAAGTGGTGGTGGCGATTCCGAAACTGGGCCCTCGTGAAGTATGGAGAAAA	6442
Qy	6121	TATGCTGGTAACATAATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6443	TATGCTGGTAACATAATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6502
Qy	6181	GGCGGCCCTCCTGTGGTGTTCCTGCATGAACCCACACAGSCATGGATCCCAAGCCCGG	6240
Db	6503	GGCGGCCCTCCTGTGGTGTTCCTGCATGAACCCACACAGSCATGGATCCCAAGCCCGG	6562
Qy	6241	CGGTTCTTGTGGAAATGTGCCCTTAAGTGTTCGAAGGAGGGAGATCAGTAGTGCATTACA	6300
Db	6563	CGGTTCTTGTGGAAATGTGCCCTTAAGTGTTCGAAGGAGGGAGATCAGTAGTGCATTACA	6622
Qy	6301	TCATCATGATATGGAAGATGTCAAGCTCTTTGCACATGAGATGGCAATCATGGTCAATGGA	6360
Db	6623	TCATCATGATATGGAAGATGTGAAGCTCTTTGCACATGAGATGGCAATCATGGTCAATGGA	6682
Qy	6361	AGGTTCCAGTGGCTTTGGCAGTCTCCAGCATCTAAAAATAGTTTGGAGATGTTTATACA	6420
Db	6683	AGGTTCCAGTGGCTTTGGCAGTCTCCAGCATCTAAAAATAGTTTGGAGATGTTTATACA	6742
Qy	6421	ATAGTTGTACGAATACGAGGGTCCAAACCCGGACCTGAGGCTGTCCAGGATTTCTTTTGA	6480
Db	6743	ATAGTTGTACGAATACGAGGGTCCAAACCCGGACCTGAGGCTGTCCAGGATTTCTTTTGA	6802
Qy	6481	CTTGCAATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATCCAGCTT	6540
Db	6803	CTTGCAATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATCCAGCTT	6862
Qy	6541	CCATCTTCATTATCTCTCTGCGCAGGATATTCAGCATCTCTCTCCAGAGCAAAAACGGA	6600
Db	6863	CCATCTTCATTATCTCTCTGCGCAGGATATTCAGCATCTCTCTCCAGAGCAAAAACGGA	6922
Qy	6601	CTCCACATAGAAGACTACTCTGTTTCTCAGACAAACATTTGACCAAGTATTTGTGAACCTT	6660
Db	6923	CTCCACATAGAAGACTACTCTGTTTCTCAGACAAACATTTGACCAAGTATTTGTGAACCTT	6982
Qy	6661	GCCAAGGACCAAGTGATGATGACCACTTTAAAGACCTCTCATTTACACAAAACAGACA	6720
Db	6983	GCCAAGGACCAAGTGATGATGACCACTTTAAAGACCTCTCATTTACACAAAACAGACA	7042
Qy	6721	GTAGTGGACGTTGCAGTCTCCACATCTTTTCTACAGGATGAGAAGTGAAGAAAGCTAT	6780
Db	7043	GTAGTGGACGTTGCAGTCTCCACATCTTTTCTACAGGATGAGAAGTGAAGAAAGCTAT	7102
Qy	6781	GTAT 6784	
Db	7103	GTAT 7106	

RESULT 7	
AAf92835	AAf92835
ID	AAf92835 standard; DNA; 7860 BP.
XX	XX
XX	AC
XX	AAf92835;
XX	XX
DT	17-MAY-2001 (first entry)
XX	XX
XX	Human ABC1 cDNA.
XX	XX
KW	High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss.
XX	XX
XX	Homo sapiens.
OS	XX
XX	XX
PN	WC200115676-A2.
XX	XX
PD	08-MAR-2001.

XX	01-SEP-2000; 2000WO-IB01492.
XX	01-SEP-1999; 99US-0151977.
XX	15-MAR-2000; 2000US-0526193.
PR	23-JUN-2000; 2000US-0213958.
XX	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(XENO-) XENON GENETICS INC.
XX	Hayden MR, Brooks-Wilson AR, Pimstone SN, Cleese SM;
XX	WPI; 2001-244356/25.
XX	Treating a lower than normal high density lipoprotein-cholesterol
PT	(HDL-C) level, a higher than normal triglyceride level, or a
PT	cardiovascular disease, by administering a compound that modulates LXR-
PT	or RXR-mediated transcriptional activity -
XX	Disclosure; Fig 2; 317pp; English.
PS	The present invention relates to a method for treating a patient
CC	diagnosed as having a lower than normal high density
CC	lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC	triglyceride level, or a cardiovascular disease, involving
CC	administering a compound that modulates LXR- or RXR-mediated
CC	transcriptional activity or ABCI expression or activity.
CC	The LXR gene product may be used in an assay to identify
CC	compounds useful for the treatment of a disease or condition selected a
CC	lower than normal HDL cholesterol level, a higher than normal
CC	triglyceride level, and a cardiovascular disease.
XX	Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;
SQ	
Query Match 99.98; Score 6776; DB 22; Length 7860;	
Best Local Similarity 99.98; Pred. No. 0;	
Matches 6779; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Oy	1 ATGGCTTTCGCGCTACGCTAGGTGTTGCTGTGGAAAGAACCTCACATTCAGAAGAAGA 60
Dd	75 ATGGCTTTCGCGCTACGCTAGGTGTTGCTGTGGAAAGAACCTCACATTCAGAAGAAGA 134
Oy	61 CAACAATGTCAGTGTTACTGGAAGTGCCTGGCCCTATTATCTCCTGATCTGATC 120
Dd	135 CAACAATGTCAGTGTTACTGGAAGTGCCTGGCCCTATTATCTCCTGATCTGATC 194
Oy	121 TCTGTGGCTGAGCTACCCACCCTATCAACAACATGAATGCCATTTCCAAAATAAAGCC 180
Dd	195 TCTGTGGCTGAGCTACCCACCCTATCAACAACATGAATGCCATTTCCAAAATAAAGCC 254
Oy	181 ATGCCCTCTGCAGGAACACTTCTTGGGTTGAGGGGATTATCTGTAATGCCAACACCCC 240
Dd	255 ATGCCCTCTGCAGGAACACTTCTTGGGTTGAGGGGATTATCTGTAATGCCAACACCCC 314
Oy	241 TGTTTCGTTACCGACATCTTGGGGAGCTCCCGAGTGTGGTGAACCTTTACAAATCC 300
Dd	315 TGTTTCGTTACCGACATCTTGGGGAGCTCCCGAGTGTGGTGAACCTTTACAAATCC 374
Oy	301 ATTGTGGCTCGCCTGTTCTCAGATCTCGGAGGCTTTTATATACAGCCAGAAAGACACC 360
Dd	375 ATTGTGGCTCGCCTGTTCTCAGATCTCGGAGGCTTTTATATACAGCCAGAAAGACACC 434
Oy	361 AGCATGAAGGACATCCGGAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 420
Dd	435 AGCATGAAGGACATCCGGAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 494
Oy	421 AACTTGAAGCTTCAAGATTTCTGTGGTGACATGAACCTTCTCTGGGTTCCTATATCAC 480
Dd	495 AACTTGAAGCTTCAAGATTTCTGTGGTGACATGAACCTTCTCTGGGTTCCTATATCAC 554
Oy	481 AACCTCTCTCCCCAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCAATCTCCAC 540
Dd	555 AACCTCTCTCCCCAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCAATCTCCAC 614

Db 2775 ATTGAGAACTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCCTGGCA 2834
QY 2761 CTGAATTTTATGAGGGCCAGATACCTCCCTTCCTGGGCCCAATGAGGGGGGAAGACG 2820
Db 2835 CTGAATTTTATGAGGGCCAGATACCTCCCTTCCTGGGCCCAATGAGGGGGGAAGACG 2894
QY 2821 ACCACCATGCTCAATCTGACCGGGTGTCCCGCCGACCTCGGGCACCGCCTACATCTCTG 2880
Db 2895 ACCACCATGCTCAATCTGACCGGGTGTCCCGCCGACCTCGGGCACCGCCTACATCTCTG 2954
QY 2881 GGAAAGACATTCGCTCTGAGATGAGCAGCACCATCCGCGCAAGACCTCGGGGCTGTCCCCAG 2940
Db 2955 GGAAAGACATTCGCTCTGAGATGAGCAGCACCATCCGCGCAAGACCTCGGGGCTGTCCCCAG 3014
QY 2941 CATACGCTGCTGTGACATGCTGACTGTGCGAAGACACATCTGTTCTATGCCCGCTTG 3000
Db 3015 CATACGCTGCTGTGACATGCTGACTGTGCGAAGACACATCTGTTCTATGCCCGCTTG 3074
QY 3001 AAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTGT 3060
Db 3075 AAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTGT 3134
QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATGACAGAAAG 3120
Db 3135 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATGACAGAAAG 3194
QY 3121 CTATCTGTGGCCTTGCCCTTCTCGGGGATCTAAGTTGTCTATCTGATGAACCCACA 3180
Db 3195 CTATCTGTGGCCTTGCCCTTCTCGGGGATCTAAGTTGTCTATCTGATGAACCCACA 3254
QY 3181 GTGTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA 3240
Db 3255 GCTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA 3314
QY 3241 GCGCGCACCATTTACTCTCTACACACACATGGATGAAGCGGACGTCTCGGGGACAGG 3300
Db 3315 GCGCGCACCATTTACTCTCTACACACACATGGATGAAGCGGACGTCTCGGGGACAGG 3374
QY 3301 ATTGCCATCATCTCCATCGGAGCTGTGTGTGGGCTCTCCCTGTTCTGAAGAAC 3360
Db 3375 ATTGCCATCATCTCCATCGGAGCTGTGTGTGGGCTCTCCCTGTTCTGAAGAAC 3434
QY 3361 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3420
Db 3435 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3494
QY 3421 TCCTGCAGAAACAGTAGTAGCTGTCTACCTGAAAGAGGAGGACAGTGTTCCTCAG 3480
Db 3495 TCCTGCAGAAACAGTAGTAGCTGTCTACCTGAAAGAGGAGGACAGTGTTCCTCAG 3554
QY 3481 AGCAGTTCTGATGCTGGCCTGGCAGCGACCATGAGAGTGACACGCTGACCATGCGATGTC 3540
Db 3555 AGCAGTTCTGATGCTGGCCTGGCAGCGACCATGAGAGTGACACGCTGACCATGCGATGTC 3614
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTCTGAAGCCGGCTGGTGAAGACATA 3600
Db 3615 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTCTGAAGCCGGCTGGTGAAGACATA 3674
QY 3601 GGGCATCAGCTGACCTATGTGTGTCATATGAAGCTGTCAAGGAGGAGGAGCCCTTTGSGAA 3660
Db 3675 GGGCATGAGCTGACCTATGTGTGTCATATGAAGCTGTCAAGGAGGAGGAGCCCTTTGSGAA 3734
QY 3661 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
Db 3735 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3794
QY 3721 GAGACGACCTGGAAGAAATATTCCTCAAGGTGGCGGAAGAGAGTGGGGTGAATGCTGAG 3780
Db 3795 GAGACGACCTGGAAGAAATATTCCTCAAGGTGGCGGAAGAGAGTGGGGTGAATGCTGAG 3854
QY 3781 ACCTCAGATGGTACCTTTGCCAGCAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3840

Db 3855 ACCTCAGATGGTACTTCCAGCAAGCAAGCAAGCGGGGCTTTCGGGCAACACGACGAGC 3914
QY 3841 TGTCTTCCCGTTCACCTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3900
Db 3915 TGTCTTCCCGTTCACCTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3974
QY 3901 GAATCCAGAGACAGACTTCTCAGTGGGATGATGGCAAGGCTCTACCAAGTGA 3960
Db 3975 GAATCCAGAGACAGACTTCTCAGTGGGATGATGGCAAGGCTCTACCAAGTGA 4034
QY 3961 GGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAAGACTGCTAATTTGCC 4020
Db 4035 GGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAAGACTGCTAATTTGCC 4094
QY 4021 AGACGGAGCTCGGAAGGATTTTGTCTCAGATTTGTGTCAGCTGTGTTTGTCTGCAAT 4080
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QY 4081 GCCCTTGTCTCAGCCTGATGCTGCCACCTTTTGGCAAGTACCCAGCCTGGAATTCAG 4140
Db 4155 GCCCTTGTCTCAGCCTGATGCTGCCACCTTTTGGCAAGTACCCAGCCTGGAATTCAG 4214
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Db 4215 CCTTGGATGTACAGCAACAGTACATTTTGTCTCAGCAATGATGCTCTCTGAGGACACGGGA 4274
QY 4201 ACCCTGGAACTTAAAGCCCTCACCAAGACCTTGGGACCCGCTGTATGGAA 4260
Db 4275 ACCCTGGAACTTAAAGCCCTCACCAAGACCTTGGGACCCGCTGTATGGAA 4334
QY 4261 GGAACCCCAATCCCAAGACACGCGCTTCCAGGAGGGAGAGAGTGAACACTTGCCTCCA 4320
Db 4335 GGAACCCCAATCCCAAGACACGCGCTTCCAGGAGGGAGAGAGTGAACACTTGCCTCCA 4394
QY 4321 GTTCCCAAGACCATCATGAGCTCTTCCAGATGGGAATCGACAATCGAACCCCTTCA 4380
Db 4395 GTTCCCAAGACCATCATGAGCTCTTCCAGATGGGAATCGACAATCGAACCCCTTCA 4454
QY 4381 CTTGATGCCAGTGTAGCAGCGACAAAATCAAGAAAGTGTGCTGCTGTGTCTCCCGCAGG 4440
Db 4455 CTTGATGCCAGTGTAGCAGCGACAAAATCAAGAAAGTGTGCTGCTGTGTCTCCCGCAGG 4514
QY 4441 GCAGGGGGCTGCTTCCCAAGAAACAAACACTGCGATATCTCTCAGGACCTG 4500
Db 4515 GCAGGGGGCTGCTTCCCAAGAAACAAACACTGCGATATCTCTCAGGACCTG 4574
QY 4501 ACAGGAAGAAACATTCGATTTATCTGTTGAGAGCTATGTGCAATCATAGCCAAAAGC 4560
Db 4575 ACAGGAAGAAACATTCGATTTATCTGTTGAGAGCTATGTGCAATCATAGCCAAAAGC 4634
QY 4561 TTAAAGAACAGATCTGGTGAATGATTTAGGTATGGGGCTTTTCCCTGGGTGTGAGT 4620
Db 4635 TTAAAGAACAGATCTGGTGAATGATTTAGGTATGGGGCTTTTCCCTGGGTGTGAGT 4694
QY 4621 AATCTCAAGCACTTCCCTCCGAGTCAAGAAATTAATGATGCTCAAAACAAATGAAGAA 4680
Db 4695 AATCTCAAGCACTTCCCTCCGAGTCAAGAAATTAATGATGCTCAAAACAAATGAAGAA 4754
QY 4681 CACCTAAAGCTGGCAAGACAGTCTGAGATCGATTTCTCAACAGCTTGGGAGATTT 4740
Db 4755 CACCTAAAGCTGGCAAGACAGTCTGAGATCGATTTCTCAACAGCTTGGGAGATTT 4814
QY 4741 ATGACAGGACTGACACAGAAATTAATGCAAGTGTGTTTCAATAACAAAGGCTGGCAT 4800
Db 4815 ATGACAGGACTGACACAGAAATTAATGCAAGTGTGTTTCAATAACAAAGGCTGGCAT 4874
QY 4801 GCAATCAGCTCTTCTGATGATCTCAACAAATGCAATGCTCCGGGCCAACCTGCAAAAG 4860
Db 4875 GCAATCAGCTCTTCTGATGATCTCAACAAATGCAATGCTCCGGGCCAACCTGCAAAAG 4934
QY 4861 GGAGAGAACCTTAGCCATTTAGTGTCTTCTCAATCATCCCTGATCTCACCAG 4920
Db 4935 GGAGAGAACCTTAGCCATTTAGTGTCTTCTCAATCATCCCTGATCTCACCAG 4994

QY 4921 CAGCAGCTCTCAGAGGTGCTCTGATGACCATCAGTGGATGCTCTGTGTCCTATCTGT 4980
 Db 4995 CAGCAGCTCTCAGAGGTGCTCTGATGACCATCAGTGGATGCTCTGTGTCCTATCTGT 5054
 QY 4981 GTCATCTTTGCAATGTCCTGCTCCAGCAGCTTGTGCTATCTCTGATCCAGAGCGG 5040
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 Db 6855 GTAT 6858

RESULT 8
 AAF83826
 ID AAF83826 standard; DNA; 7860 BP.
 XX AAF83826;
 XX AAF83826;
 DT 06-AUG-2001 (first entry)
 XX Human ABC1 nucleotide sequence.
 XX ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
 XX LDL; ds.
 OS Homo sapiens.
 XX Key
 FH Location/Qualifiers

75..3341
/*tag= a
/product= "partial ABC1 protein"
/note= "the coding sequence continues beyond nucleotide
3341, possibly till position 6860 as identified
by translating the present sequence; part of the
corresponding protein is missing and nucleotide
3341 corresponds to the last amino acid residue
(position 1089) as indicated in the
specification"

WO200132184-A2.
10-MAY-2001.
01-NOV-2000; 2000WO-US30109.
01-NOV-1999; 99US-0162803.
30-JUN-2000; 2000US-0215564.
(WISC) WISCONSIN ALUMNI RES FOUND.
Attie AD, Cook M, Gray-Keller MP, Hayden MR, Pimstone S;
Brooks-Wilson A;
WPI: 2001-335779/35.
P-PSDB; AAB62691.
New method for inhibiting cholesterol uptake in the gut comprises
administration of an inhibitor of an ABC1 protein -
Disclosure; Page 34-36; 41pp; English.
The invention relates to a new method for inhibiting cholesterol uptake
in the gut that comprises administration of an inhibitor of an ABC1
protein. The method is useful for: lowering levels of LDL (low density
lipoprotein) cholesterol by reducing the activity of ABC1 protein in the
intestinal cells and the abundance of the ABC1 protein in the individual
by inhibiting the activity of the protein; identifying drugs that can
lower serum cholesterol and LDL levels comprises assaying the drug to
test if it can bind to an ABC1 protein; testing LDL cholesterol lowering
agents; and for modulation of ABC1 biological activity. The present
sequence represents a human ABC1 nucleotide sequence.

Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;
Query Match 99.8%; Score 6772.8; DB 22; Length 7860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6777; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 61 CARACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTATCTTCCTGATCCTGATC 120
Db 135 CAACAATGTCACTGCTGCTGGAAGTGGCCTGGCCTCTATTATCTTCCTGATCCTGATC 194
QY 121 TCTGTTCCGGCTGAGCTACCCACCCCTATGAACAATGAATGCCATTTTCCAAATAAAGCC 180
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QY 241 TGTGTTCCGTTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTTGAAACTTTAAACAAATCC 300
Db 315 TGTGTTCCGTTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTTGAAACTTTAAACAAATCC 374
QY 301 ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCAGAAAGACAC 360
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Db 2175 GTGGTCACTCCTGAAGTATAGAAACCTGCTGCCCTACAGTATCCAGCGTGGTGTGTC 2234
QY 2161 TTCCTGTCCGTGTTTGTGTGTGTAATTCCTGCACTGCTGCTGCTGATAGCACATCTTC 2220
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 Db 6015 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGAIGCCATCACAGAGCTG 6074
 QY 6001 TTGACTGGGAGAGAACACGTGGAGTCTTTTGGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6060
 Db 6075 TTGACTGGGAGAGAACACGTGGAGTCTTTTGGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6134
 QY 6061 GTTGGCAAGGTTGGTGAAGTGGGCGATTGGAAACTGGGCTCGTGAAGTATGGAGAAAAA 6120
 Db 6135 GTTGGCAAGGTTGGTGAAGTGGGCGATTGGAAACTGGGCTCGTGAAGTATGGAGAAAAA 6194
 QY 6121 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
 Db 6195 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6254
 QY 6181 GCGGGGCTCCTGCTGTGTTTCTGGATGAACCCACACAGGATGATCCCAAGCCCGG 6240
 Db 6255 GCGGGGCTCCTGCTGTGTTTCTGGATGAACCCACACAGGATGATCCCAAGCCCGG 6314
 QY 6241 CGGTTCTGTGGAATGTGCGCTTAAGTGTGTCAAGGGGGAGATCAGTAGTCTTACA 6300
 Db 6315 CGGTTCTGTGGAATGTGCGCTTAAGTGTGTCAAGGGGGAGATCAGTAGTCTTACA 6374
 QY 6301 TCTCATAGTATGAAGAATGTGAAGTCTTCTGACATAGGATGCAATCATGTCATGGA 6360
 Db 6375 TCTCATAGTATGAAGAATGTGAAGTCTTCTGACATAGGATGCAATCATGTCATGGA 6434
 QY 6361 AGGTTCCAGTGGCTTGGCAGTGTCCAGCATCTAAATAATAGGTTTGGAGATGTTTACA 6420
 Db 6435 AGGTTCCAGTGGCTTGGCAGTGTCCAGCATCTAAATAATAGGTTTGGAGATGTTTACA 6494
 QY 6421 ATAGTTGTACGATACAGGTTCCACCGGACCTGAAGCCTGTCCAGGATTTCTTGA 6480
 Db 6495 ATAGTTGTACGATACAGGTTCCACCGGACCTGAAGCCTGTCCAGGATTTCTTGA 6554
 QY 6481 CTGTGATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACATACCAAGCTT 6540
 Db 6555 CTGTGATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACATACCAAGCTT 6614
 QY 6541 CCATCTTCATTAATCTCTGCGCAGGATATTCAGCATCCTCTCCAGAGCAAAAGCGA 6600
 Db 6615 CCATCTTCATTAATCTCTGCGCAGGATATTCAGCATCCTCTCCAGAGCAAAAGCGA 6674
 QY 6601 CTCACATAGAAAGACTACTCTCTCTCAGACACACATGACCAAGTATTTGTGAACCTT 6660
 Db 6675 CTCACATAGAAAGACTACTCTCTCTCAGACACACATGACCAAGTATTTGTGAACCTT 6734
 QY 6661 GCCAAGGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6720
 Db 6735 GCCAAGGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6794
 QY 6721 GTAGTGGAGTGTGAGTGTCTACATCTTTTCTACAGGATGAGAAAGTCAAAAGAGCTAT 6780
 Db 6795 GTAGTGGAGTGTGAGTGTCTACATCTTTTCTACAGGATGAGAAAGTCAAAAGAGCTAT 6854
 QY 6781 GTAT 6784
 Db 6855 GTAT 6858
 RESULT 9
 AAD21326
 ID AAD21326 standard; DNA; 7260 BP.
 XX

AC AAD21326;
 XX DT 28-JAN-2002 (first entry)
 XX DE Human ATP binding cassette transporter 1 (ABCI) gene.
 KW Human; ATP binding cassette transporter 1; ABCI; coronary heart disease;
 KW dermatological; atherosclerosis; cardiovascular; inflammatory disease;
 KW psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
 KW immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
 OS Homo sapiens.
 XX FH Location/Qualifiers
 FT CDS 321..7106
 FT /*tag= a
 FT /*product= "Human ABCI protein"
 XX PN EP1136552-A1.
 XX PD 26-SEP-2001.
 XX PF 20-MAR-2000; 2000EP-0105820.
 XX PR 20-MAR-2000; 2000EP-0105820.
 XX PA (FARB) BAYER AG.
 XX PI Schmitz G, Bodzioch M;
 XX WPI: 2001-640388/74.
 XX P-PSDB; AAE13022.
 XX New adenosine triphosphate binding cassette transporter-1 gene
 XX polymorphisms, useful for diagnosing and treating lipid disorders,
 XX cardiovascular diseases and inflammatory diseases
 XX Example 1; Fig 1; 48pp; English.
 CC The invention relates to four common polymorphisms in the gene encoding
 CC ATP-binding cassette transporter-1 (ABCI). ABCI is associated with
 CC decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
 CC ABCI directly affects cellular lipid homeostasis, which is a key factor
 CC in the atherogenetic processes. The ABCI polymorphisms are useful for
 CC diagnosing and treating lipid disorders, cardiovascular diseases
 CC (coronary heart disease, atherosclerosis) and inflammatory diseases
 CC (psoriasis, lupus erythematosus). The identification of ABCI as a
 CC transporter for interleukin-beta (IL-1beta) identifies this gene as
 CC a candidate for treatment of inflammatory diseases including rheumatoid
 CC arthritis and septic shock. The present sequence is human ABCI gene.
 XX SQ Sequence 7260 BP; 1834 A; 1765 G; 1905 G; 1756 T; 0 other;

Query Match 99.8%; Score 6768; DB 22; Length 7260;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 6774; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ATGGCTTTGTTGGCTCAGCTGAGTGTCTGCTGTGGAGAACCTCAGTTTCAGAGAGA 60
 Db 321 ATGGCTTTGTTGGCTCAGCTGAGTGTCTGCTGTGGAGAACCTCAGTTTCAGAGAGA 380
 QY 61 CAACATGTGAGCTGTTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 120
 Db 381 CAACATGTGAGCTGTTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 440
 QY 121 TCTGTTCCGGCTGAGCTACCCACCTATGACACATCAATGCCATTTCCTCAATAAGCC 180
 Db 441 TCTGTTCCGGCTGAGCTACCCACCTATGACACATCAATGCCATTTCCTCAATAAGCC 500
 QY 181 ATGCCCTCTCCAGAACACTTCTTGGGTTTCAGGGGATATCTGTATGCCAACACCCG 240
 Db 501 ATGCCCTCTCCAGAACACTTCTTGGGTTTCAGGGGATATCTGTATGCCAACACCCG 560

Qy	241	TGTTTCCGTTACCCGACNTCTCGGGAGGCTCCCGAGTCTTCTTGGAACCTTTACAAATCC	300
Db	561	TGTTTCCGTTACCCGACNTCTCGGGAGGCTCCCGAGTCTTCTTGGAACCTTTACAAATCC	620
Qy	301	ATTGTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAGACACC	360
Db	621	ATTGTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAGACACC	680
Qy	361	AGCATGAAGGACATCGCCAAAGTTCTTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	420
Db	681	AGCATGAAGGACATCGCCAAAGTTCTTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	740
Qy	421	AACCTGAAGCTTCAAGATTCTCTGCTGGACAAATCAAACTTCTCTGGTTCCTTATATCAC	480
Db	741	AACCTGAAGCTTCAAGATTCTCTGCTGGACAAATCAAACTTCTCTGGTTCCTTATATCAC	800
Qy	481	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGTGTGAGGGCTGATGTCTTCCTCAC	540
Db	801	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGTGTGAGGGCTGATGTCTTCCTCAC	860
Qy	541	AAGGTATTTTTCGAAGGCTACCAGTTACATTGTGCAAGTCTGTGCAATGATCAAAATCA	600
Db	861	AAGGTATTTTTCGAAGGCTACCAGTTACATTGTGCAAGTCTGTGCAATGATCAAAATCA	920
Qy	601	GAAGACATGATTCAACTTGGTCAACAAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	660
Db	921	GAAGACATGATTCAACTTGGTCAACAAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	980
Qy	661	AAACTGGCTGCAGAGAGGAGTACTTCGTTCCAACTATGACATCTCTGAGGCCAATCTCTG	720
Db	981	AAACTGGCTGCAGAGAGGAGTACTTCGTTCCAACTATGACATCTCTGAGGCCAATCTCTG	1040
Qy	721	AGAACACTAAACTCTACATCTCCCTCCCGAGCAGGAGCTGGCTGAAGCCACAAAACA	780
Db	1041	AGAACACTAAACTCTACATCTCCCTCCCGAGCAGGAGCTGGCTGAAGCCACAAAACA	1100
Qy	781	TTGCTGCAATAGTCTGGGACTCTGGCCGAGGAGTGTTTACGATCGAAGCTGGAGTGAC	840
Db	1101	TTGCTGCAATAGTCTGGGACTCTGGCCGAGGAGTGTTTACGATCGAAGCTGGAGTGAC	1160
Qy	841	ATGCGACAGGAGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCACAAATC	900
Db	1161	ATGCGACAGGAGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCACAAATC	1220
Qy	901	TACCAGGCTGTGTCCTGATTTGTCTCGGGGATCCCGAGGAGGGGGCTGAGATCAAG	960
Db	1221	TACCAGGCTGTGTCCTGATTTGTCTCGGGGATCCCGAGGAGGGGGCTGAGATCAAG	1280
Qy	961	TCCTCAACTGGTATGAGGACACAACTACAAGCCCTCTTTGAGGCAATGSCACTGAG	1020
Db	1281	TCCTCAACTGGTATGAGGACACAACTACAAGCCCTCTTTGAGGCAATGSCACTGAG	1340
Qy	1021	GAAGATGCTGAACCTTCTTATGACAACTCTACAATCCTTACTGCAATGATTGATGAAG	1080
Db	1341	GAAGATGCTGAACCTTCTTATGACAACTCTACAATCCTTACTGCAATGATTGATGAAG	1400
Qy	1081	AANTTGGAGTCTAGTCTCTTTTCCCGCATTTCTTGGAAGCTCTGAGCCGCTGCTCGTT	1140
Db	1401	AANTTGGAGTCTAGTCTCTTTTCCCGCATTTCTTGGAAGCTCTGAGCCGCTGCTCGTT	1460
Qy	1141	GGGAAGATCTCTGATACACTGACACTCCAGCCACAAAGCAGGTCAATGGCTGAGGTCAAC	1200
Db	1461	GGGAAGATCTCTGATACACTGACACTCCAGCCACAAAGCAGGTCAATGGCTGAGGTCAAC	1520
Qy	1201	AAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAATCAGC	1260
Db	1521	AAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAATCAGC	1580
Qy	1261	CCCAAGATCTGGACCTTCATGGAGACACCCAGAAATGGACCTTGTCCGGATCTCTGTG	1320
Db	1581	CCCAAGATCTGGACCTTCATGGAGACACCCAGAAATGGACCTTGTCCGGATCTCTGTG	1640
Qy	1321	GACAGCAGGACATGACCACTTTTGGGAACACAGCAGTTGGATGGCTTAGATTGACAGCC	1380

Db	1641	GACAGCAGGACAATGACCACTTTTGGAAACGACAGTTGGATGGCTTAGATTTGGACAGCC	1700
Qy	1381	CAAGACATCGTGGCGSTTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATAGTTCT	1440
Db	1701	CAAGACATCGTGGCGSTTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATAGTTCT	1760
Qy	1441	GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACCAAGCAATACCAAGGCAATCCGGACCATATCTCG	1500
Db	1761	GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACCAAGCAATACCAAGGCAATCCGGACCATATCTCG	1820
Qy	1501	TTTCATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1560
Db	1821	TTTCATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1880
Qy	1561	AACAAGTCCATGGAGCTGCTGATGAGAGGAGTCTTGGGTGCTGATTTGTTGTCACTGGGA	1620
Db	1881	AACAAGTCCATGGAGCTGCTGATGAGAGGAGTCTTGGGTGCTGATTTGTTGTCACTGGGA	1940
Qy	1621	ATTACTCCAGGAGCAATTGAGCTGCCCATCATGATCTCAAGTACAAAGATCCGAATGGACATT	1680
Db	1941	ATTACTCCAGGAGCAATTGAGCTGCCCATCATGATCTCAAGTACAAAGATCCGAATGGACATT	2000
Qy	1681	GACAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGGACCTGTGCTCTGAGCT	1740
Db	2001	GACAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGGACCTGTGCTCTGAGCT	2060
Qy	1741	GACCCCTTTGAGACATGGGTACGCTCTGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1800
Db	2061	GACCCCTTTGAGACATGGGTACGCTCTGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	2120
Qy	1801	GAGCAGGCAATCATCAGGTGCTGACGGGCAACCGAGAGAAAACCTGGTGCTATATGCAA	1860
Db	2121	GAGCAGGCAATCATCAGGTGCTGACGGGCAACCGAGAGAAAACCTGGTGCTATATGCAA	2180
Qy	1861	CAGATGCCCTATCCCTGTACCTTGTGATGACATCTTTCTCGGGGTGATGAGCGGTCAATG	1920
Db	2181	CAGATGCCCTATCCCTGTACCTTGTGATGACATCTTTCTCGGGGTGATGAGCGGTCAATG	2240
Qy	1921	CCCTCTTTCATGACGTGGCGCTGGATTTACTCAGTGGGTGATCATCAAGGGCATCGTG	1980
Db	2241	CCCTCTTTCATGACGTGGCGCTGGATTTACTCAGTGGGTGATCATCAAGGGCATCGTG	2300
Qy	1981	TATGAGAGGAGCAGCGCTGAAGAGAGCAATCGCGATCATCGGCTCGGACAAAGAGATA	2040
Db	2301	TATGAGAGGAGCAGCGCTGAAGAGAGCAATCGCGATCATCGGCTCGGACAAAGAGATA	2360
Qy	2041	CTCTGGTTTAGCTGGTTTCAATTAGTAGACCTTCATCTCTTTGTGAGCGCTGGCTGCTA	2100
Db	2361	CTCTGGTTTAGCTGGTTTCAATTAGTAGACCTTCATCTCTTTGTGAGCGCTGGCTGCTA	2420
Qy	2101	GTGTGTCATCTGAAGTTAGAAACCTGCTGCCCTACAGTGATCCAGCGGTGGTGTGTC	2160
Db	2421	GTGTGTCATCTGAAGTTAGAAACCTGCTGCCCTACAGTGATCCAGCGGTGGTGTGTC	2480
Qy	2161	TTCTGTGTCGTTTGTGCTGCTGGTGCAATCTCTGCACTGCTTCTCATTTAGCACACTCTTC	2220
Db	2481	TTCTGTGTCGTTTGTGCTGCTGGTGCAATCTCTGCACTGCTTCTCATTTAGCACACTCTTC	2540
Qy	2221	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATCTACTTCAACGCTGTACTGGCCC	2280
Db	2541	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATCTACTTCAACGCTGTACTGGCCC	2600
Qy	2281	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2601	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2660
Qy	2341	CTGCTGTCTCTGTGGCTTTTGGGTTGGCTGTGAGTACTTTTGGCTTTTGGAGGAGAG	2400
Db	2661	CTGCTGTCTCTGTGGCTTTTGGGTTGGCTGTGAGTACTTTTGGCTTTTGGAGGAGAG	2720
Qy	2401	GGCATGTGAGTGGAGTGGGACAACTGTTTGAGAGTCTTGTGGAGGAGATGGCTTCAAT	2460

Db 2721 GGCATTGGAGTGCAGTGGGACAAACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTTCAAT 2780
QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTGACACACCTTCTCTATGGGTGATGACCTGG 2520
Db 2781 CTCACCACTTCGATCTCCATGATGCTGTTTGACACACCTTCTCTATGGGTGATGACCTGG 2840
QY 2521 TACATTGAGGCTGCTTTCAGGCCAGTAGGGAATTCAGGCCCTTGGTATTTTCTTCTTGC 2580
Db 2841 TACATTGAGGCTGCTTTCAGGCCAGTAGGGAATTCAGGCCCTTGGTATTTTCTTCTTGC 2900
QY 2581 ACCAAGTCTCTACTGTTTGGCAGGAAAGTATGAGAGAGACACCTGGTTCCAAACAG 2640
Db 2901 ACCAAGTCTCTACTGTTTGGCAGGAAAGTATGAGAGAGACACCTGGTTTCCAAACAG 2960
QY 2641 AAGAGAAATGTGAGAAATCTGCATGGAGGAGAACCCACCCATTGAAGTGGGCCGTGCC 2700
Db 2961 AAGAGAAATGTGAGAAATCTGCATGGAGGAGAACCCACCCATTGAAGTGGGCCGTGCC 3020
QY 2701 ATTCAAGAACTGTGTAAGTCTACCGAGATGGATGAGTGAAGTGGCTGTGATGGCCGTGCA 2760
Db 3021 ATTCAAGAACTGTGTAAGTCTACCGAGATGGATGAGTGAAGTGGCTGTGATGGCCGTGCA 3080
QY 2761 CTGAAATTTTATGAGGCCAGATCACTCTCTCTGGGCCACAATGGAGCGGGGAAGAG 3140
Db 3081 CTGAAATTTTATGAGGCCAGATCACTCTCTCTGGGCCACAATGGAGCGGGGAAGAG 3140
QY 2821 ACCACCATGCTCAATCTGACCGGGTGTTCGCCCGACCTCGGGCAGCCGCTTACATCTGT 2880
Db 3141 ACCACCATGCTCAATCTGACCGGGTGTTCGCCCGACCTCGGGCAGCCGCTTACATCTGT 3200
QY 2881 GGAAGAGCAATTCGCTGAGATGAGCAACCATCCGGCAGAACCTGGGGTCTGTCCCCAG 2940
Db 3201 GGAAGAGCAATTCGCTGAGATGAGCAACCATCCGGCAGAACCTGGGGTCTGTCCCCAG 3260
QY 2941 CATACGCTGCTTGTGACATGCTGACTGTGAGAAACACATCTGTTTCTATGCCCGTTG 3000
Db 3261 CATACGCTGCTTGTGACATGCTGACTGTGAGAAACACATCTGTTTCTATGCCCGTTG 3320
QY 3001 AAAGGCTCTCTGAGAAGCACCTGAAAGCGGAGATGGAGCAGATGGCCCTGAGTGTGGT 3060
Db 3321 AAAGGCTCTCTGAGAAGCACCTGAAAGCGGAGATGGAGCAGATGGCCCTGAGTGTGGT 3380
QY 3061 TTGCCATCAGCACTGAAAGCAAAACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3120
Db 3381 TTGCCATCAGCACTGAAAGCAAAACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3440
QY 3121 CTATCTGTGGCTTGGCTTGTGCGGGGATCTAAGGTGTGATCTGATGAAACCCACA 3180
Db 3441 CTATCTGTGGCTTGGCTTGTGCGGGGATCTAAGGTGTGATCTGATGAAACCCACA 3500
QY 3181 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGCAA 3240
Db 3501 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGCAA 3560
QY 3241 GGCSCACCATATCTCTCTACACACACATGGATGAGCGGACCTCTGGGGGACAGG 3300
Db 3561 GGCSCACCATATCTCTCTACACACACATGGATGAGCGGACCTCTGGGGGACAGG 3620
QY 3301 ATTGCCATCATCTCCATGGAAGCTGTGCTGTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3360
Db 3621 ATTGCCATCATCTCCATGGAAGCTGTGCTGTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3680
QY 3361 CAGCTGGGAACAGGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Db 3681 CAGCTGGGAACAGGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3740
QY 3421 TCCTGCGAAGAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3741 TCCTGCGAAGAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3800
QY 3481 AGCAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3801 AGCAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600

QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGAGAGCCCGCTGGTGGAGACATA 3600
Db 3861 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGAGAGCCCGCTGGTGGAGACATA 3920
QY 3601 GGCATGAGCTGACCTATGTCTGCCATATGAAGCTGTGAAGAGGAGGCTTTGTGAA 3660
Db 3921 GGCATGAGCTGACCTATGTCTGCCATATGAAGCTGTGAAGAGGAGGCTTTGTGAA 3980
QY 3661 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTAGCATCTCA 3720
Db 3981 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTAGCATCTCA 4040
QY 3721 GAGACGACCTTGGAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG 3780
Db 4041 GAGACGACCTTGGAGAAATATTCCTCAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG 4100
QY 3781 ACCTCAGATGGTACTCTGCCAGCAAGACGAAACAGGGGGCTTCGGGGACAAGCAGAGC 3840
Db 4101 ACCTCAGATGGTACTCTGCCAGCAAGACGAAACAGGGGGCTTCGGGGACAAGCAGAGC 4160
QY 3841 TGTCTTCGCGCGTTCACCTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 3900
Db 4161 TGTCTTCGCGCGTTCACCTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 4220
QY 3901 GAATCCAGAGACAGACTTCTCAGTGGATGGATGGCAAGGGTCTCTACCAAGTGA 3960
Db 4221 GAATCCAGAGACAGACTTCTCAGTGGATGGATGGCAAGGGTCTCTACCAAGTGA 4280
QY 3961 GGCTGGAACCTTACACAGCAACAGTCTTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4020
Db 4281 GGCTGGAACCTTACACAGCAACAGTCTTGTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4340
QY 4021 AGACGAGTCCGAAAGGATTTTGTCTCAGATGCTTGTGACAGTGTGTTGTCTGCATT 4080
Db 4341 AGACGAGTCCGAAAGGATTTTGTCTCAGATGCTTGTGACAGTGTGTTGTCTGCATT 4400
QY 4081 GCCCTTGTGTGACGCTGATGCTGCCACCTTTGGCAAGTACCCAGCCCTGGAACTTCAG 4140
Db 4401 GCCCTTGTGTGACGCTGATGCTGCCACCTTTGGCAAGTACCCAGCCCTGGAACTTCAG 4460
QY 4141 CCCTGATGTACAAACAGCACTACATTTGTTCAGCAATGATCTCTGAGGACACGGGA 4200
Db 4461 CCCTGATGTACAAACAGCACTACATTTGTTCAGCAATGATCTCTGAGGACACGGGA 4520
QY 4201 ACCCTGGAACCTTTAAAGCCCTCACAAAGACCTTGGCTTCGGGACCCGCTGTATGAA 4260
Db 4521 ACCCTGGAACCTTTAAAGCCCTCACAAAGACCTTGGCTTCGGGACCCGCTGTATGAA 4580
QY 4261 GGAACCCCAATCCAGACAGCCCTGCCAGGAGGAGGAGGAGTGGACCTGCCCCA 4320
Db 4581 GGAACCCCAATCCAGACAGCCCTGCCAGGAGGAGGAGGAGTGGACCTGCCCCA 4640
QY 4321 GTTCCCGAGACCATCATGAGACCTTCTTCCAGATGGAACTGGACAAATGCAACCCCTCA 4380
Db 4641 GTTCCCGAGACCATCATGAGACCTTCTTCCAGATGGAACTGGACAAATGCAACCCCTCA 4700
QY 4381 CTTGCTATGCCAGTGTAGCAGCAAAATCAAGACATGCTGCTGTGTGCTGCTGCTGCTGCT 4440
Db 4701 CTTGCTATGCCAGTGTAGCAGCAAAATCAAGACATGCTGCTGTGTGCTGCTGCTGCTGCT 4760
QY 4441 GCAGGGGGCTGCTCTCTCCAAAGAAACAAACACATGCAAGATATCTTCCAGACCTG 4500
Db 4761 GCAGGGGGCTGCTCTCTCCAAAGAAACAAACACATGCAAGATATCTTCCAGACCTG 4820
QY 4501 ACAGGAGAAACATTCGGATATCTGTTGAGACATATGTCAGATCATACGCAAAAGC 4560
Db 4821 ACAGGAGAAACATTCGGATATCTGTTGAGACATATGTCAGATCATACGCAAAAGC 4880
QY 4561 TTAAGAAACAAAGATCTGGGTGAATGATTTAGGTATGGCGGCTTTTCCCTGGGTGCTAGT 4620
Db 4881 TTAAGAAACAAAGATCTGGGTGAATGATTTAGGTATGGCGGCTTTTCCCTGGGTGCTAGT 4940

QY 841 ATGGACAGAGGATGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 900
DB 1161 ATGGACAGAGGATGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 1220
QY 901 TACCAGGCTGTCTCGTATGTTCTGCGGGCATCCGAGGAGGGGGCTGAGATCAAG 960
DB 1221 TACCAGGCTGTCTCGTATGTTCTGCGGGCATCCGAGGAGGGGGCTGAGATCAAG 1280
QY 961 TCTCTCACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
DB 1281 TCTCTCACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1340
QY 1021 GAAGATGCTGAACCTTCATGACAACTACAACTCCTTACTGCAATGATTTGATGAAG 1080
DB 1341 GAAGATGCTGAACCTTCATGACAACTACAACTCCTTACTGCAATGATTTGATGAAG 1400
QY 1081 AATTGGAGTCTAGTCTCTTCTCCGCATTTCTGGAAGCTCTGAAGCGCTGCTCGTT 1140
DB 1401 AATTGGAGTCTAGTCTCTTCTCCGCATTTCTGGAAGCTCTGAAGCGCTGCTCGTT 1460
QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGTGAAC 1200
DB 1461 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGTGAAC 1520
QY 1201 AAGACCTTCAGAACTGGCTGTGTTCCATGATCTGGAAGGATGTGGGAGGAACCTCAGC 1260
DB 1521 AAGACCTTCAGAACTGGCTGTGTTCCATGATCTGGAAGGATGTGGGAGGAACCTCAGC 1580
QY 1261 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGTCCGGATGCTGTTG 1320
DB 1581 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGTCCGGATGCTGTTG 1640
QY 1321 GACAGAGGACAAATGACCACTTTTGGGACAGCACTTGGAGGCTTACATGAGGACAGCC 1380
DB 1641 GACAGAGGACAAATGACCACTTTTGGGACAGCACTTGGAGGCTTACATGAGGACAGCC 1700
QY 1381 CAAGACATCGTGGCTTTTGGCCAAAGCAGCAGAGGATGTCAGTCCAGTAAATGTTCT 1440
DB 1701 CAAGACATCGTGGCTTTTGGCCAAAGCAGCAGAGGATGTCAGTCCAGTAAATGTTCT 1760
QY 1441 GTGTACACCTGGAGAGAGCTTTCAAGAGACTAACAGGCAATCCGGACCAATATCTCGC 1500
DB 1761 GTGTACACCTGGAGAGAGCTTTCAAGAGACTAACAGGCAATCCGGACCAATATCTCGC 1820
QY 1501 TTCAATGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1560
DB 1821 TTCAATGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1880
QY 1561 AACAACTCCATGAGGCTGTGATGAGAGAGAAATCTGGGCTGGTATGTTGTTCACTGGA 1620
DB 1881 AACAACTCCATGAGGCTGTGATGAGAGAGAAATCTGGGCTGGTATGTTGTTCACTGGA 1940
QY 1621 ATTACTCCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAAATGGACAT 1680
DB 1941 ATTACTCCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAAATGGACAT 2000
QY 1681 GACAATGTGAGGAGGACAAATAAATCAAGATGGGTACTGGGACCTGTCTCTGAGCT 1740
DB 2001 GACAATGTGAGGAGGACAAATAAATCAAGATGGGTACTGGGACCTGTCTCTGAGCT 2060
QY 1741 GACCCCTTTGAGGACATCCGGTACGTCTGGGGGCTTCGCCCTACTGACAGGATGGTG 1800
DB 2061 GACCCCTTTGAGGACATCCGGTACGTCTGGGGGCTTCGCCCTACTGACAGGATGGTG 2120
QY 1801 GAGCAGCAATCATCAGGGTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 1860
DB 2121 GAGCAGCAATCATCAGGGTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 2180
QY 1861 CAGATGCCCTATCCCTGTAGTGTGATGACATCTTCTGCGGGTGTAGCCGGTCAATG 1920
DB 2181 CAGATGCCCTATCCCTGTAGTGTGATGACATCTTCTGCGGGTGTAGCCGGTCAATG 2240
QY 1921 CCCCTCTTCATGACCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980

DB 2241 CCCCTCTTCATGAGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 2300
QY 1981 TATGAGAAAGGAGGACCGCTGAAAGAGACCATGGGATCATGGCCTGGCAACAGACATA 2040
DB 2301 TATGAGAAAGGAGGACCGCTGAAAGAGACCATGGGATCATGGCCTGGCAACAGACATC 2360
QY 2041 CTCGTGTTTACCTGGTTCATTAAGTACCTCATCTCTTCTTGTGAGGGCTGGCCTGCTA 2100
DB 2361 CTCGTGTTTACCTGGTTCATTAAGTACCTCATCTCTTCTTGTGAGGGCTGGCCTGCTA 2420
QY 2101 GTGGTCACTCCAGATAGGAAACCTGCTGCCCTACAGTATCCAGCGCTGCTGTTGTC 2160
DB 2421 GTGGTCACTCCAGATAGGAAACCTGCTGCCCTACAGTATCCAGCGCTGCTGTTGTC 2480
QY 2161 TTCTGTCCGTGTTGCTGTGGTGACAAATCCTGAGTCTTCTGATTTAGCACACTCTTC 2220
DB 2481 TTCTGTCCGTGTTGCTGTGGTGACAAATCCTGAGTCTTCTGATTTAGCACACTCTTC 2540
QY 2221 TCCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCACTACTTACACCTGTACTGCTGCC 2280
DB 2541 TCCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCACTACTTACACCTGTACTGCTGCC 2600
QY 2281 TACGTCTGTGTGGTGGCATGGCAGACTACGTGGGCTTTCACACTCAAGATTTGCTAGC 2340
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QY 2461 CTCACACTTCGATCTCCATGATGCTGTTGACACTTCTCTATGSGGTGATGACCTGG 2520
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QY 2521 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCACAGCCCTGGTATTTCTCTTGC 2580
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DB 3021 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCCTGGCA 3080
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DB 3201 GGAAGACATTCGCTCTGAGTACCCAGCAGACCTGGGGCTGTGCTGCCCGAG 3260
QY 2941 CATAAGCTGTGTTTACATGCTGACTGTGGAAGAACATCTGTTCTATGCTGCCCGTTG 3000
DB 3261 CATAAGCTGTGTTTACATGCTGACTGTGGAAGAACATCTGTTCTATGCTGCCCGTTG 3320
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Db 3321 AAAGGGCTCTGTGAGAGCACGTTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3380
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Qy 3121 CTATCTGTGCGCTTGGCTTTGCGGGGATCTAAGTTGTCTATTCTGGATGAACCCACA 3180
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Qy 3181 GCTGGTGTGACCCCTTACTCCCGCAGGGGATATGGAGCTGTCTGCTGAAATACCGACAA 3240
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 6781 GTAT 6784
 7101 GTAT 7104

RESULT 11
 AAS06120
 ID AAS06120 standard; cDNA; 9741 BP.

XX AAS06120;
 XX 12-SEP-2001 (first entry)
 XX Human ABC1 DNA sequence #1.
 XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
 XX Homo sapiens.

Key	Location/Qualifiers
FT CDS	185..6967
FT FT	/tag= a
FT FT	/product= "Human ABC1 protein"
XX	WO200130848-A2.
PN	03-MAY-2001.
XX	26-OCT-2000; 2000WO-EP10886.
XX	26-OCT-1999; 99EP-0402668.
PR	01-MAR-2000; 2000US-0186260.
XX	(AVET) AVENTIS PHARMA SA.
PI	Deneville P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;
PI	Lemoline C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
PI	Dean M;
XX	WPI; 2001-316327/33.
DR	

DR P-PSDB: AAU02176.
 XX New human ABC1 nucleic acids and polypeptides for treating
 PT atherosclerosis, malaria and diabetes -
 XX
 XX
 PS Claim 1; Page 204-208; 368pp; English.
 CC The sequence represents the coding sequence #1 of human ABC1. The
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
 CC and polypeptides and vectors are useful for the prevention of
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
 CC useful for screening for an active ingredient for the prevention or
 CC treatment of a disease resulting from dysfunction in the reverse
 CC transport of cholesterol. The nucleic acids and polypeptides are also
 CC useful for treating and preventing cardiovascular and neurological
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-
 CC cholesterol (LCAT) deficiency, malaria and diabetes.
 XX
 SQ Sequence 9741 BP: 2650 A; 2180 C; 2290 G; 2620 T; 1 other;
 Query Match 99.7%; Score 6764.8; DB 22; Length 9741;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ATGGCTTGTGGCTCAGCTGAGTTCTGCTGTGGAGAACCTCACTTTCAGAGAAGA 60
 DB 185 ATGGCTTGTGGCTCAGCTGAGTTCTGCTGTGGAGAACCTCACTTTCAGAGAAGA 244
 QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTTATCTTCCTGATCCTGATC 120
 DB 245 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTTATCTTCCTGATCCTGATC 304
 QY 121 TCTGTTCGGCTGAGCTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAGCC 180
 DB 305 TCTGTTCGGCTGAGCTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAGCC 364
 QY 181 ATGGCTCTGAGAACACATTCCTTGGTTTCAGGGATATCTGTAATGCGCAACACCC 240
 DB 365 ATGGCTCTGAGAACACATTCCTTGGTTTCAGGGATATCTGTAATGCGCAACACCC 424
 QY 241 TGTTCCTGTTACCGACTCTGCGGAGGCTCCCGGAGTGTGGAAACTTTTAAACAATCC 300
 DB 425 TGTTCCTGTTACCGACTCTGCGGAGGCTCCCGGAGTGTGGAAACTTTTAAACAATCC 484
 QY 301 ATTTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCAGAAAGACAC 360
 DB 485 ATTTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCAGAAAGACAC 544
 QY 361 AGCATGAAGGACATGCGGAAGTTCTGAGAACATTCAGCAGATCAAGAAATCCAGCTCA 420
 DB 545 AGCATGAAGGACATGCGGAAGTTCTGAGAACATTCAGCAGATCAAGAAATCCAGCTCA 604
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 DB 665 AACCTCTCTCCCAAGTCTACTGTGGAGCAAGATGCTGAGGCTGATGTCTATCTCCAC 724
 QY 541 AAGTATTTTGAAGCTACCACTTACATTTGACAGTCTGTCATGATGATCAAAATCA 600
 DB 725 AAGTATTTTGAAGCTACCACTTACATTTGACAGTCTGTCATGATGATCAAAATCA 784
 QY 601 GAAGAGATGATTAACCTTGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAAGAGAG 660
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QY 721 AGAACACTAAACTCTACATCTCCCTCCGAGCAAGAGAGCTGGCTGAAGCCACAAAACA 780
 DB 905 AGAACACTAAACTCTACATCTCCCTCCGAGCAAGAGAGCTGGCTGAAGCCACAAAACA 964
 QY 781 TTGCTGCATAGTCTTGGGACTCTGCCCCAGGAGCTGTTTACAGCATGAGAGAGCTGGAGTAC 840
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 QY 841 ATGGACAGAGAGTGTATGTTCTGACCAATGTGAACAGTCCAGCTCTCCACCCCAATC 900
 DB 1025 ATGGACAGAGAGTGTATGTTCTGACCAATGTGAACAGTCCAGCTCTCCACCCCAATC 1084
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 DB 1865 GACAAATGTCGAGAGCAATATAAATCAAGATGGTGTGAGGACCCCTGGTCTCGAGCT 1924
 QY 1741 GACCCCTTTGAGGACATGCGGTACGTCTGAGGAGGCTTCCCTTACTTTCAGGATGTGGTG 1800
 DB 1925 GACCCCTTTGAGGACATGCGGTACGTCTGAGGAGGCTTCCCTTACTTTCAGGATGTGGTG 1984
 QY 1801 GAGCAGGCAATCATGAGGTGCTGACGGGACCGAGAGAAACTGGTGTCTATATGCAA 1860

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Db 1985 GACAGGCAATCATCAGGTGCTGACGGGCACCGAGAAACCTGGTCTATATGCAA 2044
QY 1861 CAGATCCCTATCCCTGTTACGTTGATGACATCTTCTTCGGGGTGATGAGCCGGTCAATG 1920
Db 2045 CAGATCCCTATCCCTGTTACGTTGATGACATCTTCTTCGGGGTGATGAGCCGGTCAATG 2104
QY 1921 CCCTCTTATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980
Db 2105 CCCTCTTATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 2164
QY 1981 TATGAGAAGGAGCGGCTGAAAGAGACCATCGGATCATGGGCTGGACAAACAGCATATA 2040
Db 2165 TATGAGAAGGAGCGGCTGAAAGAGACCATCGGATCATGGGCTGGACAAACAGCATATA 2224
QY 2041 CTCGTGTTAGCTGGTTCATTTAGTAGCCCTCATTCCTCTTCTTGTGAGCGCTGGCTGTCTA 2100
Db 2225 CTCGTGTTAGCTGGTTCATTTAGTAGCCCTCATTCCTCTTCTTGTGAGCGCTGGCTGTCTA 2284
QY 2101 GTGGTCACTCCTGAAGTTAGAAACCTGCTGCCCTACAGTGAATCCCAAGCGTGTGTTGTC 2160
Db 2285 GTGGTCACTCCTGAAGTTAGAAACCTGCTGCCCTACAGTGAATCCCAAGCGTGTGTTGTC 2344
QY 2161 TTCTCTGCTGCTTTCCTGTGTGTGACAACTCTGCAGTGTCTCTGATTAGACACTCTTC 2220
Db 2345 TTCTCTGCTGCTTTCCTGTGTGTGACAACTCTGCAGTGTCTCTGATTAGACACTCTTC 2404
QY 2221 TCCAGAGCCAACTGGCAGCAGCGCTGTGGGGGATCATCTACTTACGCTGTACCTGCC 2280
Db 2405 TCCAGAGCCAACTGGCAGCAGCGCTGTGGGGGATCATCTACTTACGCTGTACCTGCC 2464
QY 2281 TAGCTCTGTGTGGCATGGCAGGACTAGTGGGGTTCACACTCAAGATCTTCGGTAGC 2340
Db 2465 TAGCTCTGTGTGGCATGGCAGGACTAGTGGGGTTCACACTCAAGATCTTCGGTAGC 2524
QY 2341 CTGCTGTCTCTGCTGCTTGGGTTTGGCTGTGAGTACTTTCGCCCTTTTGGAGGAGCAG 2400
Db 2525 CTGCTGTCTCTGCTGCTTGGGTTTGGCTGTGAGTACTTTCGCCCTTTTGGAGGAGCAG 2584
QY 2401 GGCATTGGAGTCAGTGGGACAACTGTTTGGAGTCCCTGTGGAGGAAAGATGCTTCAAT 2460
Db 2585 GGCATTGGAGTCAGTGGGACAACTGTTTGGAGTCCCTGTGGAGGAAAGATGCTTCAAT 2644
QY 2461 CTCACCACTTCGATCTCCATGATGCTTTTGACACCTTCTCTATGGGTGATGACCTG 2520
Db 2645 CTCACCACTTCGGTCTCCATGATGCTTTTGACACCTTCTCTATGGGTGATGACCTG 2704
QY 2521 TACATTGAGGCTGCTTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCCTTGC 2580
Db 2705 TACATTGAGGCTGCTTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCCTTGC 2764
QY 2581 ACCAAGTCTACTGCTTTGGCGAGGAAAGTGTGAGAGAGCCACCTGTTCCCAACCGAG 2640
Db 2765 ACCAAGTCTACTGCTTTGGCGAGGAAAGTGTGAGAGAGCCACCTGTTCCCAACCGAG 2824
QY 2641 AAGAGAATGCAAAATCTGATGGAGGAGAACCCACCACTTGAAGCTGGGCGTGTCC 2700
Db 2825 AAGAGAATGCAAAATCTGATGGAGGAGAACCCACCACTTGAAGCTGGGCGTGTCC 2884
QY 2701 ATTCAGAACCTGTTAAAGTCTACGAGATGGATGGAAGTGGCTGTGATGGCTTGGCA 2760
Db 2885 ATTCAGAACCTGTTAAAGTCTACGAGATGGATGGAAGTGGCTGTGATGGCTTGGCA 2944
QY 2761 CTGAATTTTATCAGGGCCAGATCACTCTCTTCTGCGCCACAAATGAGCGGGGAAGACG 2820
Db 2945 CTGAATTTTATCAGGGCCAGATCACTCTCTTCTGCGCCACAAATGAGCGGGGAAGACG 3004
QY 2821 ACCACCATGTCATCTCTGACCGGTTTGTCCCGCCGACCTCGGGCACCAGCTTACATCTG 2880
Db 3005 ACCACCATGTCATCTCTGACCGGTTTGTCCCGCCGACCTCGGGCACCAGCTTACATCTG 3064
QY 2881 GGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG 2940
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Db 3065 GGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAAACCTGGGGTCTGTCCCCAG 3124
QY 2941 CATACGCTGCTGTTGACATGCTGACTCTGCAAGAACACATCTGTTCTATGCGCGTTG 3000
Db 3125 CATACGCTGCTGTTGACATGCTGACTCTGCAAGAACACATCTGTTCTATGCGCGCTTG 3184
QY 3001 AAAGGGCTCTCTGAGAAGCAGCTGAAGCGGAGATGGAGAGATGGCCCTGGATGTTGGT 3060
Db 3185 AAAGGGCTCTCTGAGAAGCAGCTGAAGCGGAGATGGAGAGATGGCCCTGGATGTTGGT 3244
QY 3061 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAAGCCAGCTGTGAGTGGAAATGCAGAGAA 3120
Db 3245 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAAGCCAGCTGTGAGTGGAAATGCAGAGAA 3304
QY 3121 CTATCTGTGGCTTGGCCCTTGTGCGGGATCTAAGGTTGTCAATCTCGATGAACCCACA 3180
Db 3305 CTATCTGTGGCTTGGCCCTTGTGCGGGATCTAAGGTTGTCAATCTCGATGAACCCACA 3364
QY 3181 GCTGTGTGGACCCCTTACTCCCGAGGGAAATATGGGAGCTGCTGCTGAATATCGGACAA 3240
Db 3365 GCTGTGTGGACCCCTTACTCCCGAGGGAAATATGGGAGCTGCTGCTGAATATCGGACAA 3424
QY 3241 GSCCGCACCATTTATTTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG 3300
Db 3425 GSCCGCACCATTTATTTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG 3484
QY 3301 ATTGCCATCATCTCCCATGGAGCTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3360
Db 3485 ATTGCCATCATCTCCCATGGAGCTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3544
QY 3361 CAGCTGGGAACAGCTACTACCTGACCTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3420
Db 3545 CAGCTGGGAACAGCTACTACCTGACCTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3604
QY 3421 TCTCTGCAAAACAGTAGTAGCACTGTGTATACCTGAAAAGAGGAGCAGAGTGTTCAG 3480
Db 3605 TCTCTGCAAAACAGTAGTAGCACTGTGTATACCTGAAAAGAGGAGCAGAGTGTTCAG 3664
QY 3481 ACAGTTCGTGCTGGCTGGCGAGCGACCATGAGATGACACCTGACCATCGATGTC 3540
Db 3665 AGCAGTTCGTGCTGGCTGGCGAGCGACCATGAGATGACACCTGACCATCGATGTC 3724
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGTGTGAAGACATA 3600
Db 3725 TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGTGTGAAGACATA 3784
QY 3601 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGTCTAAGGAGGAGCCTTTGTGAA 3660
Db 3785 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGTCTAAGGAGGAGCCTTTGTGAA 3844
QY 3661 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTTTCATGTTATGSCATCTCA 3720
Db 3845 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTTTCATGTTATGSCATCTCA 3904
QY 3721 GAGCAGACCTTGAAGAAATATTCTCAAGGTGGCGGAGAGAGTGGGTGGATGCTGAG 3780
Db 3905 GAGCAGACCTTGAAGAAATATTCTCAAGGTGGCGGAGAGAGTGGGTGGATGCTGAG 3964
QY 3781 ACCTCAGATGGTACCTTCCAGCAAGACAGACAGCGGGCCTTGGGGACAGCAGAGC 3840
Db 3965 ACCTCAGATGGTACCTTCCAGCAAGACAGACAGCGGGCCTTGGGGACAGCAGAGC 4024
QY 3841 TGTCTTCGCGCGCTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCA 3900
Db 4025 TGTCTTCGCGCGCTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCA 4084
QY 3901 GAATCCAGAGACAGACTTGTCTAGTGGGATGGATGGCAAAAGGTCCTACCAAGTGAAA 3960
Db 4085 GAATCCAGAGACAGACTTGTCTAGTGGGATGGATGGCAAAAGGTCCTACCAAGTGAAA 4144
QY 3961 GCTGTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 4020
Db 4145 GCTGTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 4204

QY	4021	AGACGGAGTCGGAAGGATTTTTTGCTCAGATTGCTTTGCCACGTGTGTTGTCTGCATT	4080
DB	4205	AGACGGAGTCGGAAGGATTTTTTGCTCAGATTGCTTTGCCACGTGTGTTGTCTGCATT	4264
QY	4081	GCCCTTGTTTCAGCCTGATCGTGGCCACCCTTTGGCAAGTACCCACAGCTGGAACTTCAG	4140
DB	4265	GCCCTTGTTTCAGCCTGATCGTGGCCACCCTTTGGCAAGTACCCACAGCTGGAACTTCAG	4324
QY	4141	CCCTGGATGTACAAGCAACAGTACACATTTGTACGAATGATGCTCTGAGGACACGGGA	4200
DB	4325	CCCTGGATGTACAAGCAACAGTACACATTTGTACGAATGATGCTCTGAGGACACGGGA	4384
QY	4201	ACCTCGAACTCTTTAAAGCCCTTCACCAAGACCCCTGGCTTCGGAGCCCGCTGTATGGAA	4260
DB	4385	ACCTCGAACTCTTTAAAGCCCTTCACCAAGACCCCTGGCTTCGGAGCCCGCTGTATGGAA	4444
QY	4261	GGAAACCCAAATCCAGACACGCCCTTGCCAGGACGGGAGGAGTAGTGACCACTGGCCCCA	4320
DB	4445	GGAAACCCAAATCCAGACACGCCCTTGCCAGGACGGGAGGAGTAGTGACCACTGGCCCCA	4504
QY	4321	GTTCGCCAGACCATCATGACCTCTTCCAGATGGAACTGGCAATGCGAGAACCCCTTCA	4380
DB	4505	GTTCGCCAGACCATCATGACCTCTTCCAGATGGAACTGGCAATGCGAGAACCCCTTCA	4564
QY	4381	CCTGTCATGCCAGTGTAGCAGCGACAAAATCAAGAAAGTGCCTGCTGTGTCCGCCACGGG	4440
DB	4565	CCTGTCATGCCAGTGTAGCAGCGACAAAATCAAGAAAGTGCCTGCTGTGTCCGCCACGGG	4624
QY	4441	GCAGGGGGCTGCTCTCTCCACAAGAAAAACAAACACTGCAGATATCTTTCAGGACCTG	4500
DB	4625	GCAGGGGGCTGCTCTCTCCACAAGAAAAACAAACACTGCAGATATCTTTCAGGACCTG	4684
QY	4501	ACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4560
DB	4685	ACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4744
QY	4561	TTAAGAACAAAGATCTGGTGAATCAGTTTAGTATGGCGCTTTTCCCTGGGTGTCACT	4620
DB	4745	TTAAGAACAAAGATCTGGTGAATCAGTTTAGTATGGCGCTTTTCCCTGGGTGTCACT	4804
QY	4621	AATACTCAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCATCAACAAATGAAGAAA	4680
DB	4805	AATACTCAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCATCAACAAATGAAGAAA	4864
QY	4681	CACCTAAAGCTGCCAAGGACAGTTCTTCAGATCGAATTTCTCAACAGCTTGGGAAGATT	4740
DB	4865	CACCTAAAGCTGCCAAGGACAGTTCTTCAGATCGAATTTCTCAACAGCTTGGGAAGATT	4924
QY	4741	ATGACAGGACTGGACACCAAGAATAATGTCAAGTGTGGTTCATATACAGGCTGGCAT	4800
DB	4925	ATGACAGGACTGGACACCAAGAATAATGTCAAGTGTGGTTCATATACAGGCTGGCAT	4984
QY	4801	GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTTCCGGGGCCAACTGCAAAAG	4860
DB	4985	GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTTCCGGGGCCAACTGCAAAAG	5044
QY	4861	GGAGAACCCCTAGCCATTATGGAAATTAAGCTTTCAATCATGCCCTGAATCTCACCAAG	4920
DB	5045	GGAGAACCCCTAGCCATTATGGAAATTAAGCTTTCAATCATGCCCTGAATCTCACCAAG	5104
QY	4921	CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCATCAGTGGATGTCCCTGTGTCCATCTGT	4980
DB	5105	CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCATCAGTGGATGTCCCTGTGTCCATCTGT	5164
QY	4981	GTCACTTTGCAATGTCTTGTGCCAGCAGCTTTGTGCTATTCCTGATCCAGGAGCGG	5040
DB	5165	GTCACTTTGCAATGTCTTGTGCCAGCAGCTTTGTGCTATTCCTGATCCAGGAGCGG	5224
QY	5041	GTGACAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCACTACTGGCTC	5100
DB	5225	GTGACAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCACTACTGGCTC	5284

QY	5101	TCTAAATTTTGCTGGGATATGTGCAATATAGGTTGTCCCTGCCACACTGGCTATTATCATC	5160
DB	5285	TCTAATTTGCTGGGATATGTGCAATATAGGTTGTCCCTGCCACACTGGCTATTATCATC	5344
QY	5161	TTCAATCTGCTTCCAGCAGAAAGTCTATGTGTCTCCACCAATCTGCCGTGCTAGCCGCTT	5220
DB	5345	TTCAATCTGCTTCCAGCAGAAAGTCTATGTGTCTCCACCAATCTGCCGTGCTAGCCGCTT	5404
QY	5221	CTACTTTTGTGTATGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5280
DB	5405	CTACTTTTGTGTATGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5464
QY	5281	AAGATCCCGCAGCACACGCTATGTGTGCTCACCGGTGAACCTCTCATTTGGCATTAAT	5340
DB	5465	AAGATCCCGCAGCACACGCTATGTGTGCTCACCGGTGAACCTCTCATTTGGCATTAAT	5524
QY	5341	GGCAGCGTGGCCACCTTTGTGTGTGGAGCTGTTCACCGCAATAAGCTGAATAATATCAAT	5400
DB	5525	GGCAGCGTGGCCACCTTTGTGTGTGGAGCTGTTCACCGCAATAAGCTGAATAATATCAAT	5584
QY	5401	GATATCTGAACTCCGTGTTCTTTGATCTTCCACATATTTTGGCTGGGAGAGGCTCATC	5460
DB	5585	GATATCTGAACTCCGTGTTCTTTGATCTTCCACATATTTTGGCTGGGAGAGGCTCATC	5644
QY	5461	GACATGGTGAATAACACGCAATGGCTGATGCCCTGGAAAGGTTTGGGAGCAATCGCTTT	5520
DB	5645	GACATGGTGAATAACACGCAATGGCTGATGCCCTGGAAAGGTTTGGGAGCAATCGCTTT	5704
QY	5521	GTGTACACCATATCTTGGGACCTGGTGGGAGAAACCTCTTCGGCATGGCCGTGGAAGGG	5580
DB	5705	GTGTACACCATATCTTGGGACCTGGTGGGAGAAACCTCTTCGGCATGGCCGTGGAAGGG	5764
QY	5581	GTGGTGTCTCTCTCATTTACTGTCTTGATCCAGTACAGATCTTTCATCAGSCCCAGACCT	5640
DB	5765	GTGGTGTCTCTCTCATTTACTGTCTTGATCCAGTACAGATCTTTCATCAGSCCCAGACCT	5824
QY	5641	GTAATGCCAAAGCTATCTCCTCTGTAATGATGAAGATGAAGATGTGAGCGGGAAAGACAG	5700
DB	5825	GTAATGCCAAAGCTATCTCCTCTGTAATGATGAAGATGAAGATGTGAGCGGGAAAGACAG	5884
QY	5701	AGAAATCTTCATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACCAAGATA	5760
DB	5885	AGAAATCTTCATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACCAAGATA	5944
QY	5761	TATAGAAGGAAGCGGAAGCCTGCTGTGTACAGGATTTGCGTGGGCATTCCTCGTGTGAG	5820
DB	5945	TATAGAAGGAAGCGGAAGCCTGCTGTGTACAGGATTTGCGTGGGCATTCCTCGTGTGAG	6004
QY	5821	TGCTTTTGGGCTCTGGGAGTTTAATGGGCTGAAATAATCATCACTTTCAAGATGTTAAACA	5880
DB	6005	TGCTTTTGGGCTCTGGGAGTTTAATGGGCTGAAATAATCATCACTTTCAAGATGTTAAACA	6064
QY	5881	GGAGATACCACTGTTACCAGAGAGATGCTTTCCTTAACAAAAATAGTATCTTATCAAAAC	5940
DB	6065	GGAGATACCACTGTTACCAGAGAGATGCTTTCCTTAACAAAAATAGTATCTTATCAAAAC	6124
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGCTG	6000
DB	6125	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGCTG	6184
QY	6001	TTGACTGGGAGAGAACACGCTGGAGTTCTTTGGCCCTTTTGAGAGAGTCCCGCAGAGAAGAA	6060
DB	6185	TTGACTGGGAGAGAACACGCTGGAGTTCTTTGGCCCTTTTGAGAGAGTCCCGCAGAGAAGAA	6244
QY	6061	GTTGGCAAGTTGGTGAAGTGGCGAATTCGAAACTGGGCCCTCGTAAGTATGGAGAAAAA	6120
DB	6245	GTTGGCAAGTTGGTGAAGTGGCGAATTCGAAACTGGGCCCTCGTAAGTATGGAGAAAAA	6304
QY	6121	TATGCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
DB	6305	TATGCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6364
QY	6181	GGCGGGCCCTCTGTGTGTTCTCTGATGAACCCACACAGCATGGATCCCAAGAGCCCGG	6240

QY	1741	GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGGGTTTCCGCTACTTGCAGATGTGGTG	1800
Db	1925	GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGGGTTTCCGCTACTTGCAGATGTGGTG	1984
QY	1801	GAGCAGGCAATCATCAGGTGCTGACGGGCACCGAGAAAGAACTGGTGTCTATATGCAA	1860
Db	1985	GAGCAGGCAATCATCAGGTGCTGACGGGCACCGAGAAAGAACTGGTGTCTATATGCAA	2044
QY	1861	CAGATGCCCTATCCCTGTTACGTTTGATGACATCTTTCTCGGGTGATGAGCCGGTCAATG	1920
Db	2045	CAGATGCCCTATCCCTGTTACGTTTGATGACATCTTTCTCGGGTGATGAGCCGGTCAATG	2104
QY	1921	CCCCTCTTCATGAGCTGGCCCTGGATTACTCAGTGGCTGTGATCATCAGGGCATCGTG	1980
Db	2105	CCCCTCTTCATGAGCTGGCCCTGGATTACTCAGTGGCTGTGATCATCAGGGCATCGTG	2164
QY	1981	TATGAGAAGGAGGACACGGCTGAAAGAGACCATCGGGATCATGGGCTCGACAAACGATA	2040
Db	2165	TATGAGAAGGAGGACACGGCTGAAAGAGACCATCGGGATCATGGGCTCGACAAACGATA	2224
QY	2041	CTCTTGGTTTACGTGGTTTCATTAGTAGCTCATCTTCCTCTTCTTGTGAGCGCTGGCGTGCTA	2100
Db	2225	CTCTTGGTTTACGTGGTTTCATTAGTAGCTCATCTTCCTCTTCTTGTGAGCGCTGGCGTGCTA	2284
QY	2101	GTGCTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCACAGCGTGGTGTGTGC	2160
Db	2285	GTGCTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCACAGCGTGGTGTGTGC	2344
QY	2161	TTCTGTCCGTGTTTGGCTGTGGTGACAACTCCAGTGCCTTCCTGATTAGCACACTCTTC	2220
Db	2345	TTCTGTCCGTGTTTGGCTGTGGTGACAACTCCAGTGCCTTCCTGATTAGCACACTCTTC	2404
QY	2221	TCCAGAGCAACCTGCGACAGCCTGTGGGGGCATCCTACTTTCACGCTGTACTGCCCC	2280
Db	2405	TCCAGAGCAACCTGCGACAGCCTGTGGGGGCATCCTACTTTCACGCTGTACTGCCCC	2464
QY	2281	TAGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2465	TAGTCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2524
QY	2341	CTGCTGTCTCCTGTGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGTGAGACAG	2400
Db	2525	CTGCTGTCTCCTGTGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGTGAGACAG	2584
QY	2401	GGCATTTGAGTGTGAGTGGGACACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2460
Db	2585	GGCATTTGAGTGTGAGTGGGACACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2644
QY	2461	CTCACCACITCGATCTCCATGATGCTGTTTGACACCTTCCTCTATATGGGTGATGACCTGG	2520
Db	2645	CTCACCACITCGATCTCCATGATGCTGTTTGACACCTTCCTCTATATGGGTGATGACCTGG	2704
QY	2521	TACATTTGAGGCTGTCTTCCAGCGCAGTACGGAATTCCTCCAGGCCCTGTATTTTCCTTGC	2580
Db	2705	TACATTTGAGGCTGTCTTCCAGCGCAGTACGGAATTCCTCCAGGCCCTGTATTTTCCTTGC	2764
QY	2581	ACCAAGTCTCTACTGGTTTGGCGAGGAAGTGTATGAGAAGGCCACCTGGTTCCAACCAG	2640
Db	2765	ACCAAGTCTCTACTGGTTTGGCGAGGAAGTGTATGAGAAGGCCACCTGGTTCCAACCAG	2824
QY	2641	AAGAGAAITGCAGAAATCTGATGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2700
Db	2825	AAGAGAAITGCAGAAATCTGATGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2884
QY	2701	ATTGAAACCTGGTAAAAGTCTTACCAGATGGGATGAAGTGGCTGTCTGATGGCCTGGCA	2760
Db	2885	ATTGAAACCTGGTAAAAGTCTTACCAGATGGGATGAAGTGGCTGTCTGATGGCCTGGCA	2944
QY	2761	CTGAAATTTTATGAGGGCCAGTACCTTCCTCTCTGGGCCACATGAGCGGGGGAAGACG	2820
Db	2945	CTGAAATTTTATGAGGGCCAGTACCTTCCTCTCTGGGCCACATGAGCGGGGGAAGACG	3004
QY	2821	ACACACATGTCATCTGACCGGGTGTGTCCCCCGACCTCTGGGSCACCGCTACATCTCTG	2880

Db 3005 ACCACATGTAATCCTGACCGGGTTGTTCCCGGACCTCGGCACCGCCTACATCTCG 3064
QY 2881 GGAAAGACATTCGCTCTGAGATGACACCATCCGCGAGAACTCGGGCTCTGTCGCCAG 2940
Db 3065 GGAAAGACATTCGCTCTGAGATGACACCATCCGCGAGAACTCGGGCTCTGTCGCCAG 3124
QY 2941 CATACGCTGCTTTTGACATGCTGACTGTCGAGACACATCTGTTCTATGCGCGCTG 3000
Db 3125 CATACGCTGCTTTTGACATGCTGACTGTCGAGAACACATCTGTTCTATGCGCGCTG 3184
QY 3001 AAAGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGACATGGCCCTGATTTGGT 3060
Db 3185 AAAGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGACATGGCCCTGATTTGGT 3244
QY 3061 TTGCGCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGACGTGGAATGACAGAAAG 3120
Db 3245 TTGCGCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGACGTGGAATGACAGAAAG 3304
QY 3121 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTTGTCTATCTGGATGAAGCCACA 3180
Db 3305 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTTGTCTATCTGGATGAAGCCACA 3364
QY 3181 GCTGTGTGGACCCCTTACTCCCGAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA 3240
Db 3365 GCTGTGTGGACCCCTTACTCCCGAGGGGAATATGGAGCTGCTGCTGAAATACCGACAA 3424
QY 3241 GSCCGCACCATTAATCTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG 3300
Db 3425 GSCCGCACCATTAATCTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG 3484
QY 3301 ATTGCCATCATCCCATGGGAAGCTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3360
Db 3485 ATTGCCATCATCCCATGGGAAGCTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3544
QY 3361 CAGCTGGGAACAGCTACTACCTGACCTGCTCAAGAAAGTGTGGAATCCTCCCTCAGT 3420
Db 3545 CAGCTGGGAACAGCTACTACCTGACCTGCTCAAGAAAGTGTGGAATCCTCCCTCAGT 3604
QY 3421 TCTGTCAGAAACAGTAGTACACTGTGTCATACCTGAAAGAGGAGCAGTGTTCCTCAG 3480
Db 3605 TCTGTCAGAAACAGTAGTACACTGTGTCATACCTGAAAGAGGAGCAGTGTTCCTCAG 3664
QY 3481 AGCAGTTCTGATGCTGGGCTGGGAGCGACCATGAGATGACACGCTGACCATCATGATGC 3540
Db 3665 AGCAGTTCTGATGCTGGGCTGGGAGCGACCATGAGATGACACGCTGACCATCATGATGC 3724
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGAAGACATA 3600
Db 3725 TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGAAGACATA 3784
QY 3601 GGGCATGAGCTGACCTATGCTGTCATATGAAGCTGCTGAAGAGGAGCGCTTTGTGGAA 3660
Db 3785 GGGCATGAGCTGACCTATGCTGTCATATGAAGCTGCTGAAGAGGAGCGCTTTGTGGAA 3844
QY 3661 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
Db 3845 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3904
QY 3721 GAGACGACCTGGAGAAATATTCTCAAGGTGGCGGAGAGAGTGGGTGGATGCTGAG 3780
Db 3905 GAGACGACCTGGAGAAATATTCTCAAGGTGGCGGAGAGAGTGGGTGGATGCTGAG 3964
QY 3781 ACCTCAGATGGTACCTTGGCCAGCAAGCAAGCGCGGCTTCGGGGACAGCAGAGC 3840
Db 3965 ACCTCAGATGGTACCTTGGCCAGCAAGCAAGCGCGGCTTCGGGGACAGCAGAGC 4024
QY 3841 TGTCTTTCGCGGCTTCACTGAAGATGATGCTGATGCCAAATGATCTGACATAGACCCA 3900
Db 4025 TGTCTTTCGCGGCTTCACTGAAGATGATGCTGATGCCAAATGATCTGACATAGACCCA 4084
QY 3901 GAATCAGAGACAGACTTGTCTGATGGGATGGATGGCAAGGGTCTTACAGGTGAAA 3960

Db 4085 GAATCCAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAGGGTCTTACCAGGTGAAA 4144
QY 3961 GGCTGGAAACATTACACAGCAACAGATTGTTGGCCCTTTTGTGGAAAGAGACTGCTAATTGCC 4020
Db 4145 GGCTGGAAACATTACACAGCAACAGATTGTTGGCCCTTTTGTGGAAAGAGACTGCTAATTGCC 4204
QY 4021 AGACGGAGTCCGGAAGGATTTTGTCTCAGATTGCTTGCACGCTGTGTTGTCTGCTGATT 4080
Db 4205 AGACGGAGTCCGGAAGGATTTTGTCTCAGATTGCTTGCACGCTGTGTTGTCTGCTGATT 4264
QY 4081 GCCCTTGTGTTCAGCTGATCGTCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTTCAG 4140
Db 4265 GCCCTTGTGTTCAGCTGATCGTCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTTCAG 4324
QY 4141 CCCTGGATGTACACAGACAGTACACATTTGTACGCAATGATGCTCTCTGAGGACACGGGA 4200
Db 4325 CCCTGGATGTACACAGACAGTACACATTTGTACGCAATGATGCTCTCTGAGGACACGGGA 4384
QY 4201 ACCCTGGAACCTCTTAAAGCGCCCTCACCAAGACCCCTGCTTCGGGAGCCGCTGTATGGAA 4260
Db 4385 ACCCTGGAACCTCTTAAAGCGCCCTCACCAAGACCCCTGCTTCGGGAGCCGCTGTATGGAA 4444
QY 4261 GGAACCCCAATCCAGACACGCGCTGCCAGCAGGGGAGGAGAGTGGACACTTGCCTCA 4320
Db 4445 GGAACCCCAATCCAGACACGCGCTGCCAGCAGGGGAGGAGAGTGGACACTTGCCTCA 4504
QY 4321 GTTCCCCAGACCATCATGACCTCTTCCAGAAATGGGAACCTGGACAATGCAGAACCTTCA 4380
Db 4505 GTTCCCCAGACCATCATGACCTCTTCCAGAAATGGGAACCTGGACAATGCAGAACCTTCA 4564
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QY 4441 GCAGGGGGCTGCTCCTCCCAAGAAACAAACACTGCAGATATCCTTTCAGGACCTG 4500
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QY 4501 ACAGGAAGAAACATTTCCGATTATCTGCTGAAGACGTATGTCAGATCATAGCCAAAGC 4560
Db 4685 ACAGGAAGAAACATTTCCGATTATCTGCTGAAGACGTATGTCAGATCATAGCCAAAGC 4744
QY 4561 TTAAGAACACAGATCTGGTGAATGAGTTAGTATGCGGCTTTTCCCTGGGTGTCAGT 4620
Db 4745 TTAAGAACACAGATCTGGTGAATGAGTTAGTATGCGGCTTTTCCCTGGGTGTCAGT 4804
QY 4621 AATCTCAAGCACCTTCCCGAGTCAAGAAATTAATGATGCCATCAACAAATGAAGAAA 4680
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QY 4681 CACCTAAAGCTGGCCAGGACAGTCTGCAGATCGATTTCACAGCTTGGGAAGATTT 4740
Db 4865 CACCTAAAGCTGGCCAGGACAGTCTGCAGATCGATTTCACAGCTTGGGAAGATTT 4924
QY 4741 ATGACAGACTGGACACCAAGAAATTAATGTCAGGTTGGTTCAATAACAGGCTGGCAT 4800
Db 4925 ATGACAGACTGGACACCAAGAAATTAATGTCAGGTTGGTTCAATAACAGGCTGGCAT 4984
QY 4801 GCAATCAGCTCTTCTGATGTCATCAACAAATGTCCTCCGGGCAACCTGCAAAAG 4860
Db 4985 GCAATCAGCTCTTCTGATGTCATCAACAAATGTCCTCCGGGCAACCTGCAAAAG 5044
QY 4861 GGAGAGAACCCCTAGCCATTATGGAATTAATGTCAGGTTGGTTCAATAACAGGCTGGCAT 4920
Db 5045 GGAGAGAACCCCTAGCCATTATGGAATTAATGTCAGGTTGGTTCAATAACAGGCTGGCAT 5104
QY 4921 CAGCAGCTCTCAGAGGTGCTGTGATGACCAATCAGTGGATGCTTGTGTCTTCCATCTGT 4980
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QY 4981 GTCATCTTTGCAATGCTCTTCTGTCAGCCAGCCTTGTGCTATTCCTGATCCAGGACGG 5040
Db 5165 GTCATCTTTGCAATGCTCTTCTGTCAGCCAGCCTTGTGCTATTCCTGATCCAGGACGG 5224

QY 5041 GTCAGCAAGCAAAACACCTGAGTTCATCAGTGAAGCCCTGTCATCTACTGGCTC 5100
Db 5225 GTCAGCAAGCAAAACACCTGAGTTCATCAGTGAAGCCCTGTCATCTACTGGCTC 5284
QY 5101 TCTAATTTTGTCTGGGATATGTCGAATACGTTGTGCTCCGACACACTGGTCAATATCATC 5160
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QY 5161 TTCATCTGCTCCAGAGAAGTCCATGATGTCCTCCACCAATCTGCCCTGGTGAGCCCTT 5220
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QY 5221 CTACTTTTCTGTATGGGTGGTCAATCACTCACTCTCATGTACCCAGCCCTCTTGTGTTTC 5280
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QY 5461 GACATGGTGAAGAACCCAGGCAATGCTGATGCCCTGGAGAAAGTTTGGGAGAAATCGCTTT 5520
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QY 5941 ATCCATGAATACATCAAGACATGGGCTTACTGCTCCTCAGTTTGTGATGCCATCACAGAGCTG 6000
Db 6125 ATCCATGAATACATCAAGACATGGGCTTACTGCTCCTCAGTTTGTGATGCCATCACAGAGCTG 6184
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Db 6185 TTGACTGGAGAGAACAGCTGGAGTTCTTTGCCCTTTTGAGAGAGTCCCGAGAGAAAGAA 6244
QY 6061 GTTGCAAGAGTTGTGAGTGGGCGCATTCGGAACTTGGCCCTCGTGAAGTATGGAGAAAAA 6120
Db 6245 GTTGCAAGAGTTGTGAGTGGGCGCATTCGGAACTTGGCCCTCGTGAAGTATGGAGAAAAA 6304

QY 6121 TATCTCTGTTACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
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QY 6181 GCGGGGCTCTCTGTTGTTTCTGGATGAACCCACACAGGCATGGATCCAAAGCCCGG 6240
Db 6365 GCGGGGCTCTCTGTTGTTTCTGGATGAACCCACACAGGCATGGATCCAAAGCCCGG 6424
QY 6241 CGTTCTTGTGGAAATGTCGCCCTTAAGTGTGTCAAGGAGGGAGATCAGTAGTGCATTACA 6300
Db 6425 CGTTCTTGTGGAAATGTCGCCCTTAAGTGTGTCAAGGAGGGAGATCAGTAGTGCATTACA 6484
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QY 6421 ATAGTTCTAGCAATAGCAGGTCCAAACCCGACCTGAAGCCTGTCAGGATTTCTTTGGA 6480
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Db 6665 CTTCATTTCTCTGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAATACCACTT 6724
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Db 6785 CTCACATAGAAGACTACTCTGTTCTCAGACAACTTGAACCAAGTATTTGTGAACTTT 6844
QY 6661 GCGAGGACCAAGTATGATGATGACACTTAAAGAGCTCTCATTACACAAAACCCAGACA 6720
Db 6845 GCGAGGACCAAGTATGATGATGACACTTAAAGAGCTCTCATTACACAAAACCCAGACA 6904
QY 6721 GTAGTGGACCTTCAGTCTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 6780
Db 6905 GTAGTGGACCTTCAGTCTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAAGCTAT 6964
QY 6781 GTAT 6784
Db 6965 GTAT 6968

RESULT 13

AAS06121
ID AAS06121 standard; cDNA; 9854 BP.

XX AAS06121;

XX AC AC
XX XX
DT 12-SEP-2001 (first entry)

XX Human ABC1 DNA sequence #2.

XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
XX cardiovascular; neurological; Tangier disease; LCAT deficiency;
XX lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 298..7078
FT /tag= a
FT /product= "Human ABC1 protein"

XX WO200130848-A2.

XX 03-MAY-2001.
PD

XX 26-OCT-2000; 2000WO-EP10886.
 XX 26-OCT-1999; 99EP-0402668.
 PR 01-MAR-2000; 2000US-0186260.
 XX (AVET) AVENTIS PHARMA SA.
 PA Denefle P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
 PI Dean M;
 XX WPI; 2001-316327/33.
 DR P-PSDB; AAU02176.
 XX New human ABC1 nucleic acids and polypeptides for treating
 XX atherosclerosis, malaria and diabetes -
 PT Claim 1; Page 209-213; 368pp; English.
 XX The sequence represents the coding sequence #2 of human ABC1. The
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
 CC and polypeptides and vectors are useful for the prevention of
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
 CC useful for screening for an active ingredient for the prevention or
 CC treatment of a disease resulting from dysfunction in the reverse
 CC transport of cholesterol. The nucleic acids and polypeptides are also
 CC useful for treating and preventing cardiovascular and neurological
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-
 CC cholesterol (LCAT) deficiency, malaria and diabetes.
 XX Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
 SQ
 Query Match 99.7%; Score 6764.8; DB 22; Length 9854;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 1 ATGGCTGTGGCTCAGCTAGGTTGCTGCTGGAAGAACCTCACTTTCCAGAAGAAGA 60
 298 ATGGCTGTGGCTCAGCTAGGTTGCTGCTGGAAGAACCTCACTTTCCAGAAGAAGA 357
 61 CAACATGTGAGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC 120
 358 CAACATGTGAGCTGTGCTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC 417
 121 TCTGTGGCTGAGCTACCAACCTATGAACACATGATGCCATTTTCCAAATAAGCC 180
 418 TCTGTGGCTGAGCTACCAACCTATGAACACATGATGCCATTTTCCAAATAAGCC 477
 181 ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTAATGCCAACACCC 240
 478 ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTAATGCCAACACCC 537
 241 TGTTCGGTTACCGACTCTGGGAGGCTCCCGGAGTTGTTGGAAACTTTACAAATCC 300
 538 TGTTCGGTTACCGACTCTGGGAGGCTCCCGGAGTTGTTGGAAACTTTACAAATCC 597
 301 ATTGTGGCTCGCCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAGACACC 360
 598 ATTGTGGCTCGCCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAGACACC 657
 361 AGCATGAAGACATCGGCAAGTTTCAGAACATTTACAGACATCAAGAAATCCAGCTCA 420
 658 AGCATGAAGACATCGGCAAGTTTCAGAACATTTACAGACATCAAGAAATCCAGCTCA 717
 421 AACTTGAAGCTTCAAGATTTCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC 480
 718 AACTTGAAGCTTCAAGATTTCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC 777
 481 AACTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCATTTCCAC 540
 778 AACTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCATTTCCAC 837

QY 541 AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
 DB 838 AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 897
 QY 601 GAAGAGATGATTAACACTTGGTGACCAAGAGTTTCTGAGCTTTTGGGCTACCAAGAGAG 660
 DB 898 GAAGAGATGATTAACACTTGGTGACCAAGAGTTTCTGAGCTTTTGGGCTACCAAGAGAG 957
 QY 661 AAACCTGGCTGCAGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCAATCTCTG 720
 DB 958 AAACCTGGCTGCAGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCAATCTCTG 1017
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 DB 1138 ATGCGACAGAGGAGTGTATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCTCCACCCAAATC 1197
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 DB 1258 TCTCTCAACTGCTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1317
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 QY 1081 AATTTGGAGTCTAGTCTCTTCCCGCATTTCTGAAAGCTCTGAAGCCGCTGCTCGTT 1140
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 DB 1498 AAGACTTCCAGGAACTGGCTGTGTCATGATCTGGAAGGATCTGGAGGAACTCAGC 1557
 QY 1261 CCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1320
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 QY 1321 GACAGAGGGAACATGACACCTTTTGGGNAACAGAGTTGGATGGCTTAGATTTGGACAGCC 1380
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 QY 1381 CAAGACATCGTGGCGTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT 1440
 DB 1678 CAAGACATCGTGGCGTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT 1737
 QY 1441 GTGTACACTGGAGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCAATATCTGCGC 1500
 DB 1738 GTGTACACTGGAGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCAATATCTGCGC 1797
 QY 1501 TTCATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
 DB 1798 TTCATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1857
 QY 1561 AAACAAGTCCATGAGAGCTGCTGGATGAGAGGAATTTCTGGGCTGGTATTGTTGTTCACTGGA 1620
 DB 1858 AAACAAGTCCATGAGAGCTGCTGGATGAGAGGAATTTCTGGGCTGGTATTGTTGTTCACTGGA 1917

Db 4078 ACCTCAGATGGTACCTTGGCAGCAAGCAAGAACAGCGCGGCTTGGGGACAAGCAGAGC 4137
QY 3841 TGTCTTCGCGCGTCTACTGAAGATGATGCTGTGATCCAAATGATCTCAGATAGACCCA 3900
Db 4138 TGTCTTCGCGCGTCTACTGAAGATGATGCTGTGATCCAAATGATCTCAGATAGACCCA 4197
QY 3901 GAATCCAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 3960
Db 4198 GAATCCAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 4257
QY 3961 GGTGTGAATCTTACACAGAACAGTTGTGTGGCCCTTTTGTGGAAGAGATGCTAAATGGC 4020
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QY 4021 AGACGAGTGGAAAGATTTTGTCTCAGATTGTCTGCCAGCTGTGTTTGTCTGCAAT 4080
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QY 4081 GCCCTTGTGTCTCAGCTGATGTCGACCCCTTGGCAAGTACCCAGCTGGAACCTCAG 4140
Db 4378 GCCCTTGTGTCTCAGCTGATGTCGACCCCTTGGCAAGTACCCAGCTGGAACCTCAG 4437
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QY 4201 ACCCTGGAATCTTAAACGCCCTTCAACAAAGACCCCTGSGTTCGGGACCCGCTGATGGAA 4260
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QY 4741 ATGACAGGACTGGACACCAAGAAATATGTCAAGGTGTGGTTCAATTAACAGGCTGGCAT 4800
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Db 6238 ATCCATGAGTACATCAGAACATGGCTACTGCTCCTCAGTTTGTGCTCATCAGAGCTG 6297

QY 6001 TTGACTGGGAGACACACGTGGAGTCTTTGGCCCTTTTTCAGAGGAGTCCACAGAGAAAGAA 6060
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 Db 7078 GTAT 7081

RESULT 14
 AAK51683
 ID AAK51683 standard; cDNA; 7281 BP.
 XX
 AC AAK51683;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 228.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX
 OS Homo sapiens.

XX WO200157190-A2.
 PN 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US04098.
 PF
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX (HYSE-) HYSEQ INC.
 FA
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR P-PSDB; AAM78550.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 useful in diagnosis and gene therapy -
 XX
 PS Claim 1; Page 1086-1096; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 SQ Sequence 7281 BP: 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
 Query Match 99.7%; Score 6763.2; DB 22; Length 7281;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6771; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ATGCTTTGTTGGCTCAGCTGAGTTCCTGCTGTGGAAGAACCTCACTTTCAAGAAGA 60
 Db 342 ATGCTTTGTTGGCTCAGCTGAGTTCCTGCTGTGGAAGAACCTCACTTTCAAGAAGA 401
 QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 120
 Db 402 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 461
 QY 121 TCTGTTGGCTGAGCTACCCACCTCATGAACAACATGAATCCCATTTTCCAAATAAAGCC 180
 Db 462 TCTGTTGGCTGAGCTACCCACCTCATGAACAACATGAATCCCATTTTCCAAATAAAGCC 521
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ABA09200
ID ABA09200 standard; cDNA; 7086 BP.

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QY 5881 GGAGATACCACTGTTTACCAGAGGAGATGCTTTCCTTAAACAAAAATAGTATCTTATCAAC 5940
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QY 6001 TTGACTGGGAGAGAACACGTTGAGTTCCTTGGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6060
Db 6342 TTGACTGGGAGAGAACACGTTGAGTTCCTTGGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6401
QY 6061 GTTGGCAAGTTGTTGAGTGGGCGATTCGGAACCTGGGCTCGTGAAGTATGAGAGAAAA 6120
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Db 6522 GCGGCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6581
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QY 6421 ATAGTTGTACGAATAGCAGGGTCCAAACCCGACCTGAAGCCCTGTCCAGATTTCTTTGA 6480
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QY 6481 CTTGCATTTCTTGGAGTGTCTTAAAGAGAAACCCGAAACATGCTACATACCAGTT 6540
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Db 6882 CCATCTTCAATATCTTCTGCTGCCAGGATATTTCAGCATCTCTCCAGAGCAAAAGGGA 6941
QY 6601 CTTCCACATAGAAGTACTCTGTTTCTCAGCAACACTTGACCAAGTATTTGTGAACTTT 6660
Db 6942 CTTCCACATAGAAGTACTCTGTTTCTCAGCAACACTTGACCAAGTATTTGTGAACTTT 7001
QY 6661 SCCAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTACACAAAAACAGACA 6720
Db 7002 GCCAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTACACAAAAACAGACA 7061
QY 6721 GTAGTGGAGTGGAGTCTCTCATCTTTTCTACAGGATGAGAAAGTGAAGAGAAAGCTAT 6780
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QY 6781 GTAT 6784
Db 7122 GTAT 7125

XX ABA09200;
 AC
 XX
 XX
 XX 11-JAN-2002 (first entry)
 XX
 XX Human ABCAL homologue-encoding cDNA, SEQ ID NO:976.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibitor; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; anti-inflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnerary; antiulcer; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200157188-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 05-FEB-2001; 2001WO-US03800.
 XX
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX
 XX WPI; 2001-457740/49.
 DR P-PSDB; ABB11956.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 1; Page 833-835; 1963pp; English.
 XX
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides,
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibitor-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 XX novel human polypeptide of the invention.
 XX
 XX Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
 Query Match 99.7%; Score 6762.2; DB 22; Length 7086;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6770; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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 DB 304 ATGGCTTGTGGCTCAGCTGAGGTGCTGTGGTGGAGAACCTCACTTTTCAGAGAGA 363
 QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGCTATTATTCTTCCTGATCCTGATC 120
 DB 364 CAACATGTCAGCTGCTGCTGGAAGTGGCTGCTATTATTCTTCCTGATCCTGATC 423
 QY 121 TCTGTTCGGCTGAGTACCCACCTATGAACAACATGAATGCCATTTCCAATAAAGCC 180
 DB 424 TCTGTTCGGCTGAGTACCCACCTATGAACAACATGAATGCCATTTCCAATAAAGCC 483
 QY 181 ATGCCCTCTGCAGGAACACTTCTTGGTTTCAGGGGATTAATCTGTAATGCCAACACCCC 240
 DB 484 ATGCCCTCTGCAGGAACACTTCTTGGTTTCAGGGGATTAATCTGTAATGCCAACACCCC 543
 QY 241 TGTTCCTGTTACCGACTCTCTGGGAGGCTCCCGAGTGTGTGAAACTTTACAAATCC 300
 DB 544 TGTTCCTGTTACCGACTCTCTGGGAGGCTCCCGAGTGTGTGAAACTTTACAAATCC 603
 QY 301 ATTTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACACC 360
 DB 604 ATTTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACACC 663
 QY 361 AGCATGAAGGACATGCGCAAGATTCTGAGAACATTAAGCAGATCAAGAATCCAGTCA 420
 DB 664 AGCATGAAGGACATGCGCAAGATTCTGAGAACATTAAGCAGATCAAGAATCCAGTCA 723
 QY 421 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAACCTTCTCTGGTTCCTATATCAC 480
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 DB 784 AACCTCTCTCTCCCAAGCTTACTGTGGACAAAGATGCTGAGGGCTGATGATTCATCTCCAC 843
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 DB 904 GAAGAGATGATTAACCTTGGTGACCAAGAGTTTCTGAGCTTTTGTGCCCTACCAAGAGG 963
 QY 661 AAACCTGCTGACGACGAGTACTTTCGTTCCAACTGGACATCCCTGAAGCCAACTCTG 720
 DB 964 AAACCTGCTGACGACGAGTACTTTCGTTCCAACTGGACATCCCTGAAGCCAACTCTG 1023
 QY 721 AGAACACTAAACTCTACATCTCCCTCCCGAGCAAGGAGCTGGCTGAAGCCACCAAAACA 780
 DB 1024 AGAACACTAAACTCTACATCTCCCTCCCGAGCAAGGAGCTGGCTGAAGCCACCAAAACA 1083
 QY 781 TTGCTGATAGTCTTGGACTCTGGCCAGGAGCTGTTTACGATGAGAACTGGAGTGAC 840
 DB 1084 TTGCTGATAGTCTTGGACTCTGGCCAGGAGCTGTTTACGATGAGAACTGGAGTGAC 1143
 QY 841 ATGGACAGGAGGTGATGTTTCTGACCAATGTGAACAGTCCAGCTCCTCCACCCAAATC 900

1144 ATGCGCAGGAGGTGATGTTCTGACCAATGTGACAGCTCCAGCTCTCCACCCAAATC 1203
901 TACAGGCTGTGTCCTGATGTTCTGCGGGCATCCCGAGGAGGGGCTGAAATCAAG 960
1204 TACAGGCTGTGTCCTGATGTTCTGCGGGCATCCCGAGGAGGGGCTGAAATCAAG 1263
961 TCTCTCAACTGTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
1264 TCTCTCAACTGTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1323
1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1080
1324 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1383
1081 AATTTGGAGTCTAGTCCCTCTTCCCGCATATCTGGAAGCTCTGGAAGCCCTGCTCGTT 1140
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1141 GGAAGATCTCTGTATACACCTTGACACTCCAGCCACAAGCGAGGTGATGGCTGAGGTGAAC 1200
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1201 AGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGCATGTGGAGGAACCTGAGC 1260
1504 AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGCATGTGGAGGAACCTGAGC 1563
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1381 CAAGACATCTGGGCTTTTGGCCAAAGCACCAGAGGATGTCAGCTCCAGTAATGGTTCT 1440
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1984 GACAATGTGGAGGACAAATAAATCAAGGATGGGTACTGGGACCCCTGGTCTCGAGCT 2043
1741 GACCCCTTTGAGGACATGGGTACGTCTGGGGGGCTTCCCTACTTTCGAGGATGGTG 1800
2044 GACCCCTTTGAGGACATGGGTACGTCTGGGGGGCTTCCCTACTTTCGAGGATGGTG 2103
1801 GAGCAGGCAATCATCAGGCTGTGACGGCACCGAGAGAAACTGGTGTCTATATGAA 1860
2104 GAGCAGGCAATCATCAGGCTGTGACGGCACCGAGAGAAACTGGTGTCTATATGAA 2163
1861 CAGATGCCCTATCCCTGTTTACGTTGATGACATCTTTTCTGCGGGTGTGATGAGCCGGTCAATG 1920
2164 CAGATGCCCTATCCCTGTTTACGTTGATGACATCTTTTCTGCGGGTGTGATGAGCCGGTCAATG 2223
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OM nucleic - nucleic search, using sw model

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6: /cgn2.6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	430.8	6.4	5894	3	US-08-665-259-24
2	430.8	6.4	5894	3	US-08-762-500-24
3	430.8	6.4	6525	3	US-08-762-500-74
4	56	0.8	7218	1	US-08-232-463-14
5	54.4	0.8	6846	4	US-08-961-527-198
6	52.4	0.8	2726	1	US-08-461-823-1
7	52.4	0.8	4646	1	US-08-181-471-2
8	52.4	0.8	4659	2	US-08-583-276-18
9	52.4	0.8	4659	6	5206352-3
10	52.4	0.8	6505	2	US-08-793-610-5
11	52.4	0.8	9318	2	US-08-793-610-6
12	52.4	0.8	4403765	4	US-09-103-840A-2
13	52.4	0.8	4411529	4	US-09-103-840A-1
14	51.6	0.8	729	4	US-09-134-001C-995
15	51.4	0.8	2391	4	US-09-221-017B-812
16	50.8	0.7	4264	2	US-08-784-649A-1
17	50.8	0.7	4264	2	US-08-784-649A-5
18	50.2	0.7	6273	4	US-08-961-527-21
19	50	0.7	6854	4	US-09-194-905-7
20	49.4	0.7	4233	3	US-09-120-513-1
21	49.4	0.7	4233	4	US-09-450-105-1
22	49.2	0.7	795	4	US-08-961-527-264
23	49.2	0.7	4659	2	US-08-752-447-1
24	49.2	0.7	4659	4	US-09-316-167-1
25	49.2	0.7	7174	4	US-08-961-527-189
26	49	0.7	5045	4	US-09-390-721-1
27	49	0.7	5045	4	US-09-390-721-3

c	28	46.2	0.7	7218	1	US-08-232-463-14	Sequence 14, Appl
	29	45.2	0.7	23673	4	US-09-773-816-1	Sequence 1, Appl
c	30	44.2	0.7	1526	4	US-08-858-207A-34	Sequence 34, Appl
	31	44.2	0.7	12127	4	US-08-961-527-148	Sequence 148, Appl
	32	43	0.6	15567	4	US-09-627-376-3	Sequence 3, Appl
	33	42.4	0.6	1518	2	US-08-997-080-88	Sequence 88, Appl
	34	42.4	0.6	1518	2	US-08-937-362-88	Sequence 88, Appl
	35	42.4	0.6	1518	3	US-08-873-970-88	Sequence 88, Appl
	36	42.4	0.6	1518	4	US-09-095-855-88	Sequence 88, Appl
	37	42.4	0.6	1518	4	US-09-324-542-88	Sequence 88, Appl
	38	42.4	0.6	1518	4	US-09-205-426-88	Sequence 88, Appl
	39	42.2	0.6	933	4	US-09-134-001C-2350	Sequence 2350, Ap
	40	42	0.6	5717	4	US-08-961-527-102	Sequence 102, Ap
	41	41.2	0.6	900	4	US-09-134-001C-1330	Sequence 1330, Ap
c	42	41	0.6	25002	4	US-08-961-527-48	Sequence 48, Appl
	43	40.8	0.6	1971	4	US-08-838-207A-72	Sequence 72, Appl
	44	40	0.6	648	4	US-09-305-984-17	Sequence 17, Appl
	45	40	0.6	648	4	US-09-073-541A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-24
; Sequence 24, Application us/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingner, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENZYME CORPORATION
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
US-08-665-259-24
Query Match 6.4%; Score 430.8; DB 3; Length 5894;

Best Local Similarity 56.1%; Pred. No. 4.1e-122;
Matches 944; Conservative 0; Mismatches 692;
Indels 48; Gaps 5

QY	1760	GGTACGTCTGGGGGGCTTCGCCCTACTTCCAGGATGTGGTGAGCAGGCAATCATCAGGG	1819
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QY	1820	TGCTGACGGGCACCGAGA-----AGAAAACTGGTGTCTATATGCAACAGA	1864
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QY	1865	TGCCCTATCCCTGTTACGTTGATGACATCTTCTTCGGGGTGATGAGCGGTCATATGCCCC	1924
Db	675	TCCGCTACCCGCGGTTTCATCGCAGACCCCTTCTCGTGGCCATCCAGTACCAGCTGCCCC	734
QY	1925	TCTTCATGACGCTGGCGTGGATTACTAGTGGCTGCATCATCAAGGGCATCGTGATG	1984
Db	735	TGCTGCTGCTCAGCTTCACTACACCGCGCTCACATTGCCCGTGTCTGTGTGGCAGG	794
QY	1985	AGAAGAGGCACGGCTGAAGACACATCGGCATCGGCCTGGACAACAGCATACTCT	2044
Db	795	AGAAGAAAGAGGCTGAAGAGTAGTACATCGCATATGGGCTCAGCAGTGGCTGCACCT	854
QY	2045	GGTTTAGCTGGTTCACTAGCGCTCATCTCTTCTGTGAGCGCTGGCCTGCTAGTGG	2104
Db	855	GGAGTGCCTGGTTCCTTGTGTTCTTCTCTCATCGCGCGCTCCTTCATGACCC	914
QY	2105	TCATCCTGAAGTTA-----GGAAACCTCTGCCCTACAGTCACTCCACGCG	2149
Db	915	TGCTCTCTGTGTCAGAGTGAAGCCAAATGTAGCGGTGCTGTCCGCGAGCGACCCCTCC	974
QY	2150	TGNGTGTTCCTTCCTGCTCGTGTTCGTGTGGTGACAACTCTGCAGTGTCTCTGATTA	2209
Db	975	TGTTGTGCGCTTCCTGCTGTGCTTCGGCATCTCTACCATCTCTCAGGTTTCATGGTCA	1034
QY	2210	GCACACTCTTCTCCAGAGCCAACTGGCAGCAGCGCTGTGGGGGCATCATCTACTTCA	2269
Db	1035	GCACCTTCTTCAGMAAGCCAACTAGCAGCAGCGCTTCGGAGGCTTCTCTACTTCTCA	1094
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QY	2330	TCTTCGCTAGCCTGTGTCCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTT	2389
Db	1155	TCGTCTCTGCCTCCTGTCTAATGTGCGCATGGCAATGGGAGCCAGCTCATTTGGGAAT	1214
QY	2390	TTGAGGACGAGGGCATTGGAGTGAGTGGGACACCTTGTGTGAGATCTCTGTGGAGAG	2449
Db	1215	TTGAGCGAAAGCATGGGCATCCAGTGGCAGACACTCCTGAGTCCCGTCAACGTGGAG	1274
QY	2450	ATGGCTTCAATCTCACCACTTCGATCTCCATGATGCTGTGTGACACTTCTCTATGGG	2509
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QY	2510	TGATGACCTTGTATATGAGGCTGTCTTTCAGGCCAGTACGGAATTCGAGGCCCTGTG	2569
Db	1335	TGGTAGCCTTGTATGAGGCGGCTCTTCCAGGGCAAGTTCGGCGTGCCTCAGCCCTGTG	1394
QY	2570	ATTTTCTTTCACCAAGTCTCTACTGGTTTGGCGAGGAAGTGTG-----AGAA	2620
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QY	2621	GCCACCTGGTTCCAAACAGAGAAGATGTGAGAAATCTGCATGGAGGAGGAACCAACC	2680
Db	1455	AAGAAGACAGTGACCCCGAGAAAGCACTCAGAAACAGGAGTACTTTGAAGCGGAGG	1514
QY	2681	ACTTGAAGCTGGGCGTGTCCATTCAGAACCTGGTAAAAGTCTACCGAGATGGATGA--	2738
Db	1515	ACCTGGTGGCGGGATCAAGATCAAGCACTGTCCAAGGTGTTCAGGTTGGGAATAGG	1574
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Db	1575	ACAGGGGGCGTCAGAGACCTGAAACCTCAACCTGTACGAGGACAGATCACCGTCCTGC	1634
Qy	2795	TGGCCCAACATGGAGCGGGGAAGACACACACCATGTCATCTCTGACCGGTTGTTCGCC	2854
Db	1635	TGGCCACACAGGTGCCGGGAACACACACCTCTCCATGCTCAAGGTCTCTTCCGC	1694
Qy	2855	CGACCTCGGCACCGOOTACATCCTCGGAAAGACATCGCTCTGAGATGACACCATCC	2914
Db	1695	CCACCAGTGGACGGCATACATCAGCGGGTATGAAATTTCCACGACATGGTTCAGATCC	1754
Qy	2915	GGCAGAACCTGGGGTCTGCCCCACGATAACGTGCTGTTTACATGCTGACTGTCGAG	2974
Db	1755	GGAAAGCCTGGGCGTGTGCCCCACGACGATCCTGTTTGACAACTTCAGACTCGACG	1814
Qy	2975	AACACATCTGGTTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACCTGAAGCGGAGA	3034
Db	1815	AGCACCTTTATTTCTACGCCACGCTGAAGGGCTGTCAAGTCAAGAGTGCCCTGAAGAG	1874
Qy	3035	TGGAGCAGATGGCCCTGGATGTTGGTTTGGCATCAAGACAGCTGAAAGCAAAACAAGCC	3094
Db	1875	TCRAGCAGATG---CTGCACATCATCGGCTCGAGGACAAGTGGAACTCACGGAGCGCT	1931
Qy	3095	AGCTGTCAAGTGGAAATGCAGAGAAAGCTATCTGGCCCTTGGCCCTTCTCGGGGATCTA	3154
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Db	1992	AGGTGTGTGATACTGGACGAGCCACCTCTGGGATGGAGCCCATCTCCAGGAGGCCATCT	2051
Qy	3215	GGAGTGTCTGTGAAATACCGACAGGCCGACACATATTCTCTCTACACACACATGG	3274
Db	2052	GGATCTTCTTAGCGCGAAGAAATGACCGCACCATCGTCTGACACCCCACTTCATGG	2111
Qy	3275	ATGAAGCGGACGTCCTGGGGGACAGATGGCATCATCTCCATGGGAAGCTGTCTGTG	3334
Db	2112	ACGAGGCTGACCTGCTGGGAGACCGATCGCCATCATGGCCAAAGGGGAGCTGCAGTCT	2171
Qy	3335	TGGGCTCTCCCTGTTCTGGAAGAACCCAGCTGGGAACAGGCTACTACCTGACCTTGCTCA	3394
Db	2172	CGGGTCTCTCGCTGTCTTCTCAAGCAGAAATACGGTGGCGGCTATCATAGCTGCTGTA	2231
Qy	3395	AGAA 3398	
Db	2232	AGGA 2235	

RESULT 2

```

RESULI 2
US-08-762-500-24
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klingner, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES.
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:

```

```

1 COMPANY: GENZYME CORPORATION
2 ADDRESS: One Mountain Road
3 STREET: One Mountain Road
4 CITY: Framingham
5 STATE: Massachusetts
6 COUNTRY: United States of Amer
7 ZIP: 01701
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent In Release #1

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> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/08/762.500
> FILING DATE: 09-DEC-1996
> CLASSIFICATION: 435
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 08/665,259
> FILING DATE: 17-JUN-1996
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: PCT/US96/10469
> FILING DATE: 17-JUN-1996
> ATTORNEY/AGENT INFORMATION:
> NAME: Dugan, Deborah A.
> REGISTRATION NUMBER: 37,315
> REFERENCE/DOCKET NUMBER: IGS-9.3
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (508) 872-8400
> TELEFAX: (508) 872-5415
> INFORMATION FOR SEQ ID NO: 24:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 5894 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: cDNA
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 2..5053
> US-08-762-500-24

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[illegible]

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QY	2450	ATGGCTTCAATCTCACCACTTCGATCTCCATGATGCTGTTTTGACACCTTCTCTATGGGG	2509
Db	1275	ACGACTTCTGCTTCGGGCAAGTGTCTGGGATGCTGCTGSACTCTGTCTCTATGGCC	1334
QY	2510	TGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATWCCAGGCCCTTGT	2569
Db	1335	TGTTGACCTGGTACATGAGGCGGTCTTCCCAGGCGAGTTCGGGCTGCCTCAGGCCCTTGT	1394
QY	2570	ATTTTCTTGCACCAAGTCTTACTGGTTTGGCGAGGAAGTAGT-----AGAAGA	2620
Db	1395	ACTTCTTCATCATGCOCTCTTATTGGTGTGGGAAGCCAAGSGGTTGCAGGGAAGGAG	1454
QY	2621	GCCACCTTGGTCCAACAGAGAGAANTGTGAGAAATCTGCATGGAGGAGAACCCACC	2680
Db	1455	ANGAAGACAGTGAOCCCGAAGAAGACACTCAGAAACGAGTACTTTGAAGCGCAGCCAGAG	1514
QY	2681	ACTTTGAAGCTGGGCGTGTCCATTTCAGAACCCTGGTAAAAAGTCTACCGAGATGGGATGA--	2738
Db	1515	ACCTGGTGGCGGGATCAAGATCAAGCACTGTCCAAGTGTTCAGGGTGGAAATAAGG	1574
QY	2739	----GGTGGCTGTGNATGGCCTGGCACTGAATTTTTATGAGGGCCAGATCACTCTCTTC	2794
Db	1575	ACAGGCGGCCCTCAGAGACTTGAACCTCAACTGTACGAGGAGACAGTACCGTCTCTGC	1634
QY	2795	TGGGCACAAATGAGGGGGAAGACGACACCATGTCAAATCTCTGACCGGGTGTCTCCCC	2854
Db	1635	TGGGCCAACACGGTGCCGGGAAGACCAACCCCTCTCCATCTCAGTGTCTTTTCCCC	1694
QY	2855	CGACCTCGGCGACCGCCTACATCTCTGGAAAAGACATTCGCTCTGAGATGAGCACTCC	2914
Db	1695	CCACCAGTGGACGGGCATACATCAGCGGTATGAAATTTCCAGGACATGGTTCAGATCC	1754
QY	2915	GGCAGAACCTGGGGTCTCTCCCCAGCATACGTGCTGTTTGACATGCTGACTGTCTGAAG	2974
Db	1755	GGAAAGCTGGGCGTGTCCCGCAGACGACATCTGTTTGACAACTTTGACAGTCTCAGCTC	1814
QY	2975	AACACATCTGGTTCTATGCCGCTTGAAGAGGCTCTCTGAGAAGCAGCTGAAGCGGAGA	3034
Db	1815	AGCACCTTTATTTACGCCAGCTGNAAGGCGCTGTACGCTCAGAGTGGCCITGAAGAAG	1874
QY	3035	TGAGACAGATGGCCCTGGATGTTGGTTTGGCCATCAAGCAAGCTGAAAGCAAAACAAGCC	3094
Db	1875	TCAAGCAGATG---CTGCACTCATCTGGCCTGGAGGACAAGTGAACCTCAGCGAGCGCT	1931
QY	3095	AGCTGTCAAGTGAATGCAGAAAAGCTATCTGTGGCCTTGGCCTTGTCTGGGGGATCTA	3154
Db	1932	TCCTGAGGGGGCATGAGCGCAAGCTCTCCATCGGCATCGCCCTCATCGCAGCTCCA	1991
QY	3155	AGGTGTGTCATCTTGGATGAACCCACAGCTGGTGTGGACCTTACTCCGCGAGGGGAATAT	3214
Db	1992	AGGTGTGATCTAGGACGACCCCACTCGGGCATGGAGCCCATCTCCAGSAGGCCATCT	2051
QY	3215	GGGAGTGTCTGCTGAATATCCGACAAGGCCGACCATTTCTCTCTACACACACATGG	3274
Db	2052	GGATCTTCTTACGGCGGAGAAAGTGAACCGGACCATCTGCTGTACCMCCACTTCAIAG	2111
QY	3275	ATGAAGCGGACGCTCTGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTG	3334
Db	2112	ACGAGGCTACCTGTCTGGGAGACGATCGCCATCATGGCCAAGGGGAGGTGCAGTGCT	2171
QY	3335	TGGGCTCTCCCTGTTTCTTAAGAACACGCTGGGACAGGCTACTACCTGACCTTGCTCA	3394
Db	2172	GCGGGTCTGCTGTGTTCTCTCAAGCAGAAATACGGTGGCGGCTATCACATGACGTGTGA	2231
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Db 2232 AGGA 2235

RESULT 3

US-08-762-500-74

; Sequence 74, Application US/08762500

; Patent No. 6030806

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/762,500

; FILING DATE: 09-DEC-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/665,259

; FILING DATE: 17-JUN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10469

; FILING DATE: 17-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6525 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 573..5684

US-08-762-500-74

Query Match 6.4%; Score 430.8; DB 3; Length 6525;

Best Local Similarity 56.18; Pred. No. 4.4e-122;

Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

QY 1760 GGTACGCTGGGGGGCTTCGCTACTTGCAGAGTGTGGTGGAGCGCAATCATCAGG 1819

Db 1186 GGTACATCGGGAAGCTTCTCGCGCGTGCAGCATGCTGTGGACCGGCATCATGGAGT 1245

QY 1820 TCGTACCGGCGCCAGCA- - - - - AGAAACTGGTGTCTATATGCAACAGA 1864

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QY 1925 TCTTCATGACGCTGGCGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATGCTGTATG 1984

Db 1366 TGTGCTGCTGCTCAGCTTCACCTACACCGCGCTCACATTGCCGCTGTGTGCTGCAGG 1425

QY 1985 AGAAGGAGGACGCGCTGAAAGAGACCATGGGATCATGGGCGCTGGCAACAGCATACTCT 2044

Db 1426 AGAAGGAAAGGAGGCTGAAGAGTACATGCGCATGATGGGCTCAGCAGCTGCTGCACT 1485

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QY 2105 TCATCCTGAAGTTA- - - - - GAAACCTGCTGGCTACAGTGATCCCGAGG 2149

Db 1546 TGTCTTCTGTGCAAGGTGAAGCAATGTAGCCGCTGCTCCGCGAGCGACCCCTCC 1605

QY 2150 TGGTGTGCTGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2209

Db 1606 TGTGCTGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665

QY 2210 GCACACTCTTCTCCAGAGCAACCTGSCAGCAGCTGCTGGGGCATCATCTACTTCCAGC 2269

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QY 2330 TCTTCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2389

Db 1786 TCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1845

QY 2390 TTGAGGAGCAGGCGATTGGAGTGCAGTGGGACCAACCTGTTTGGAGTCTCTGTGGAGAG 2449

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QY 2855 CGACCTCGGCGCCCTACATCTCTGGGAAACACATTCGCTCTGAGATGAGCACCATCC 2914

Db 2326 CCACAGTGGAGCGGATACATCAGCGGTATGAAATTTCCAGAGGACATGGTTCAGATCC 2385

QY 2915 GGCAGACCTGGGGGCTGTGCTCCCGAGCATAACTGCTGTTTGGACATGCTGACTGTGGAAG 2974

Db 2386 GGAAGACCTGGGCGCTGTGCGCGCAGCAGACATCTCTGTTTGACAACTTGACAGTCCAG 2445

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgt-Fls
; US-08-232-463-14

Query Match          0.8%; Score 56; DB 1; Length 7218;
Best Local Similarity 5.6%; Pred No. 5,8e-06;
Matches 23; Conservative 221; Mismatches 166; Indels 0; Gaps

QY 4930 TCAGAGGTGGCTGTGATGACCATCAGTCAGGATGTCCTTGTCCTCATCTGTGTCATCTTT 4989
      || || ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1050 TCGAGGGAGCTTGGCATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1109

QY 4990 GCAATGTCCTTCGTCCACCGACGCTTGTGCTATTCTGTATCCAGGAGCGGGTCAGCAA 5049
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1110 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1169

QY 5050 GCAAAACACTGCAGTTCATCAGTGGAGTGAGCTGCATCTACTGGCTCTCTAATTTT 5109
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Db 1170 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1239

QY 5110 GTCTGGGATATGCAATTACGTTGTCCCTGCCACATGGTCATTATCATCTTCATCTGC 5169
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Db 1230 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1389

QY 5170 TTCCAGCAGATCCTATGTGCTCCACCAATCTGCTGTAGCCCTCTCTACTTTTG 5229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1290 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1349

QY 5230 CTGTATGGGTGTCATACACTCTCATGTACCAGCGCTCTTGTTGTTCAAGATCCOC 5289
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1350 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1409

QY 5290 AGCACAGCCTATGTGTGCTCACCAGCGGTGAACCTCTTCATTGGCATTA 5339
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1410 YYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAATCTCTCTATCTCTTTAA 1459

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RESULT 5
US-08-961-527-198/c
Sequence 198, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.373

Query Match	0.98;	Score 52.4;	DB 1;	Length 4646;
Best Local Similarity	46.7%;	Pred. No. 5.5e-05;		
Matches 253; Conservative	0;	Mismatches 271;	Indels 18;	Gaps 2;
QY	2750	ATGSCCTGGCACTGAATTTTATCAGGCGCCAGATCACTCTCTCTGCGGCCACCAATGGAG	2809	
DB	3585	AGGACCTGAGCTGGAGGTGAAGAAGGCCAGACGCTGGCTCTGGTGGCAGCAGCTGGCT	3644	
QY	2810	CGGGAAAGACAGACCACCATGTCAATCTGACCCGGTGTGTTCCTCCCGACCTCGGGCACCG	2869	
DB	3645	GTGGAAAGAGCACAGTGGTCCAGCTCTGGTGGAGCGGTTCTACGACCCCTTGGCAGGAAAG	3704	
QY	2870	CTACATCTCTGGGAAAAGACAT--TCGCTCTGAGATGAGCACCATCGGCAGAACCTGG	2925	
DB	3705	TGCTGCTGTATGGCAAGAAATAAAGCGCATGAATTTCACTGGCTCGAGCACACCTGG	3764	
QY	2927	GGGTCTGTCCCCAGCAAAACGTGTGTGTGACATGCTGACTGTGTGAAGAACAACATCTGGT	2985	
DB	3765	GCATCGTGTCCAGGACCCATCTCTGTTGACTGCAGCATTTGCTCAGAACATTGCCTATG	3824	
QY	2987	TCTATGCCGCTTGAAGGGCTCTCTGAGAAGCAGCTGAAGCGGAGATGGAGCAGATGG	3046	
DB	3825	GAGACACAGCGGGTGGTGTACAGGAAGAAGATCGTGAAGGCGACAAAGGAGGCCAACA	3884	
QY	3047	CCCTGGATGTGTGGTGTGCCATCAAGCAAGCTGAAGAAG-----CAAACAA	3091	
DB	3885	TACATGCCCTTCATCGAGTCACTGCTATAATAATATAGCACTAAAGTAGAGACAAAGAA	3944	
QY	3092	GCCAGCTGTCAAGTGGAAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTGGGGGAT	3151	
DB	3945	CTCAGCTCTCTGGTGGCCAGAAACCCATTGCCATAGCTCGTGCCTTGTATTAGACAGC	4004	
QY	3152	CTAAGTTGTCTATCTTGGATGAACCCAGCTGGTGTGGACCTTACTTCCCGCAGGGAA	3211	
DB	4005	CTCATATTTTGTCTTTGGATGAAGCCACGTCAGCTCTGTGATACAGAAAGTGAAAGAGTTG	4064	
QY	3212	TATGGGAGCTGCTGTGAAATACCCACAGGCCCGACCATATTCTCTCTACACACCACA	3271	
DB	4065	TCCAAGAAGCCCTGGACAAAGCCAGAGAAGGCCCGCACTGTCATTGTGATGTCTCACCGCC	4124	
QY	3272	TG 3273		

Query Match	0.8%; Score 52.4; DB 2; Length 4669;
Best Local Similarity	46.7%; Pred. No. 5.5e-05;
Matches 253; Conservative	0; Mismatches 271; Indels 18; Gaps 12;

QY	2750	ATGGCGCTGGCACTGAATTTTATGAGGGCCAGATCACCTCTTCCTGGCCCATGTGAG	2809
Dd	3585	AGGGACTAGCCTGGAGGTGAAGAAGGCCAGACGCTGCCTGTGTGGCAGCAGTGCT	3644
QY	2810	CGGGAAAGACGACCACCATGTCAAATCCCTGACCGGGTGTTCGCCCGCACCTCGGGCAACG	2869
Dd	3645	GTTGGGAAGACGACATGTTCTCGAGCTCTCTGGACCGGTTCTACGACCCCTTGGCAGGGAAAG	3704
QY	2870	CCTACATCCTTGGGAAAAGACAT---TCGCTCTGAGATGAGCACCATCCGGCAGAACCTGG	2926
Dd	3705	TGCTGCTTGAATGGCAAGAAATAAAGCGACTCAATGTTTCAGTGGCTCCGAGCACACCTGG	3764
QY	2927	GGGTGTGCCCCAGCATACGTGCTGCTGTTTGACATGCTGACTGTCAAGAACACATCTGCT	2986
Dd	3765	GCATCGTGTCCCAGGAGGCCATCCTGTTTGACTGTCAGCATTTGCTGAGAACATTGGCTATG	3824
QY	2987	TCTATGCGCGCTTGAAGAGGGCTCTCTGAGAAGCACGCTGAAGCGGAGATGGAGCAGATGG	3046
Dd	3825	GACACAACACCGCGGTGGTGTCACAGGAACAGATCGTAGGGCCAGCAAGGAGGCCAAC	3884
QY	3047	CCCTGGATGTGGTTGGCATCAAGCAAGCTGAAAAG-----CAAACAA	3091

Db	4005	CTCATATTTTGCCTTTTGGATGAAGCCACGTCAGCTCGATACAGAAAGTGAAGAAGTTG	4064
QY	3212	TATGGGAGCTGCTGCTGAATACCGACAAGCGCGACCAATTATTCTCTCTACACACCACA	3271
Db	4065	TCCNAGAGCCCTGGACAGCCAGGAAGGCGGCACCTGCATTGTGTGATGTCACGCC	4124
QY	3272	TG	3273
Db	4125	TG	4126

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RESULT 10
US-08-793-610-5
; Sequence 5, Application US/08793610
; Patent No. 5858744
; GENERAL INFORMATION:
; APPLICANT: BAUM, Christopher
; APPLICANT: STOCKING-HARRERS, Carol
; APPLICANT: OSTERTAG, Wolfram
; TITLE OF INVENTION: RETROVIRAL VECTOR
; TITLE OF INVENTION: FOR GENE TRANSFER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Nikaido, Marmelstein, Murray & Orsini
 STREET: 655 Fifteenth Street N.W. Suite 330
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/793,610
 FILING DATE: 07-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 31 973.8
 FILING DATE: 08-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 195 03 952.1
 FILING DATE: 07-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP95/03175
 FILING DATE: 10-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Berman, Richard J.
 REGISTRATION NUMBER: 39,105
 REFERENCE/DOCKET NUMBER: P1614-7007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)638-5000
 TELEFAX: (202)638-4810
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6505 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA
 US-08-793-610-5

	Query Match	0.8%	Score 52.4;	DB 2;	Length 6505;
	Best Local Similarity	46.7%;	Prod. No. 7e-05;		
	Matches 253;	Conservative	0;	Mismatches 271;	Indels 18; Gaps 2;
QY	2750	ATGGCGCTGGCACTGAATTTTATCAGGGCCAGATACCTCTCTTCCTGGGCCCAATGGAS	2809		
Ddb	4977	AGGGACTAGCCTGGAGGTGAAGAAAGGCCACAGCGTGGCTCTGTGGGCGAGCAGTGGCT	5036		
QY	2810	CGGGGAAGACGACCAACCATGTCAATCTCTACCGGGTTTGTCCCCCGGAGCTCGGGGCACCG	2869		

Db 5037 GTGGGAAGACACAGTGGTCCAGCTCCTGGAGCGGTTCTACGACCCCTTGGCAGGGAAG 5096
 QY 2870 CTTACATCCTGGGAAAGACAT---TCGCTCTGAGATGAGCACCACCTGCGGAGACCTGG 2926
 Db 5097 TGTGCTTGTATGCAAGAAATAAGCGACTGAATGTTTCAGTGGCTCCGAGCAGACCTGG 5156
 QY 2927 GGTGCTGTCGCCAGCATAACGTGCTCTTTGACATGCTGACTGTGGAAGAACACATCTGCT 2986
 Db 5157 GATGCTGTCGCCAGGAGCCCTCTTTGACTGCGAGCATGCTGAGACATGCTGCTATG 5216
 QY 2987 TCTATGCCGCTTGAAGGGCTCTCTGAGAGACACGTGAAGCGGAGATGGAGCAGATGG 3046
 Db 5217 GAGACAAACAGCCGGTGGTGTACAGGAAGAGATCGTAGGGCAGCAAGAGGAGGCAACA 5276
 QY 3047 CCTGTGATGTTGTTGCCATCAAGCAAGCTGAAG-----CAAAACAA 3091
 Db 5277 TACATGCCCTTCATCGAGTCACTGCCCTTAATAATATAGCACTAAAGTAGGAGCAAGGAA 5336
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 Db 5337 CTCAGCTCTGCTGGCCAGAAACAGCATTGCCATAGCTGCTGCCCTTGTAGACAG 5396
 QY 3152 CTAAGTTGTCATCTGGATGACCCACAGCTGGTGTGACCCCTTACTCCCGCAGGGGA 3211
 Db 5397 CTCATATTTTGTCTTTGGATGAAGCCACGCTACGCTCTGGATACAGAAAGTGAAGGTTG 5456
 QY 3212 TATGGAGCTGCTGCTGAATACCGACAGCGCGGACCATTAATCTCTTACACACACA 3271
 Db 5457 TCCAGNAGCCCTGGACAAAGCAGAGAGCGCGGACCTGCTGATGCTGCTACCGCC 5516
 QY 3272 TG 3273
 Db 5517 TG 5518

RESULT 11
 US-08-793-610-6
 ; Sequence 6, Application US/08793610
 ; Patent No. 5858744
 ; GENERAL INFORMATION:
 ; APPLICANT: BAUM, Christopher
 ; APPLICANT: STOCKING-HARBERS, Carol
 ; APPLICANT: OSTERTAG, Wolfram
 ; TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram LLP
 ; STREET: 655 Fifteenth Street N.W. Suite 330
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,610
 ; FILING DATE: 07-MAR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 44 31 973.8
 ; FILING DATE: 08-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 195 03 952.1
 ; FILING DATE: 07-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP95/03175
 ; FILING DATE: 10-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bertram, Richard J.
 ; REGISTRATION NUMBER: 39,105

REFERENCE/DOCKET NUMBER: PI614-7007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)638-5000
 TELEFAX: (202)638-4810
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9318 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA
 US-08-793-610-6
 Query Match 0.8%; Score 52.4; DB 2; Length 9318;
 Best Local Similarity 46.7%; Pred. No. 9.2e-05;
 Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
 QY 2750 ATGGCTTGGCCTGATTTTATGAGGGCCAGATCACTCTCTCTCGGGCCACATGAG 2809
 Db 4936 AGGGACTGAGCTGGAGGTGAAGAAGGGCCAGACCTGGCTGTGGTGGCAGCAGTGGCT 4995
 QY 2810 CGGGGAAGACGACACCATGTCAATCCCTGACCGGGTGTTCCTCCCGGACCTCGGCACCG 2869
 Db 4996 GTGGGAAGACGACAGTGTCCAGCTCCTGGAGCGGTCTACGACCCCTTGGCAGGGAAG 5055
 QY 2870 CTTACATCCTGGGAAAGACAT---TCGCTCTGAGATGAGCACCATCCGGCAGAACCTGG 2926
 Db 5056 TGTGCTTGTATGCAAGAAATAAAGCGACTGAATGTTTCAGTGGCTCCGAGCAGACCTGG 5115
 QY 2927 GGGTGTGTCGCCAGCATAACGTGCTGTTTACATGCTGACTGTGAAAGAACACATCTGCT 2986
 Db 5116 GCATCTGTCCCGAGGAGCCATCCCTGTTTACTGTCAGCATGCTGAGAACATGCTGCTATG 5175
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 QY 3047 CCTGTGATGTTGTTTGGCTCAAGCAAGCTGAAG-----CAAAACAA 3091
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 Db 5356 CTCATATTTTGTCTTTGGATGAAGCCACGCTGAGTCTGATACAGAAAGTGAAGGTTG 5415

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 429.143 Seconds
(without alignments)
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Perfect score: 6784
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	6766.4	99.7	9870	9	US-09-984-827-97
3	6766.4	99.7	9870	9	US-09-984-827-101
4	6766.4	99.7	9870	9	US-09-984-827-103
5	6766.4	99.7	9870	9	US-09-984-827-105
6	6764.8	99.7	9741	10	US-09-846-456-10
7	6764.8	99.7	9870	9	US-09-984-827-92
8	6764.8	99.7	9870	9	US-09-984-827-93
9	6764.8	99.7	9870	9	US-09-984-827-94
10	6764.8	99.7	9870	9	US-09-984-827-115
11	6764.8	99.7	9870	9	US-09-984-827-119
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15	6764.8	99.7	9870	9	US-09-984-827-123
16	6764.8	99.7	9870	9	US-09-984-827-124
17	6764.8	99.7	9870	9	US-09-984-827-125
18	6764.8	99.7	9870	9	US-09-984-827-126
19	6763.2	99.7	9741	9	US-09-984-827-1

ALIGNMENTS

RESULT 1

US-09-984-827-95
Sequence 95, Application US/09984827
Publication No. US2003005623A1
GENERAL INFORMATION:
APPLICANT: DENEFELE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 9870
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (7138)
OTHER INFORMATION: a, t, c or g

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGCCTCAGCTGAGTTGCTGCTGGGAAGAACCTCACTTTCAGAAGA 60

314 ATGGCTTTGGCCTCAGCTGAGTTGCTGCTGGGAAGAACCTCACTTTCAGAAGA 373

QY 61 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCCTATTATCTCTGATCCTGATC 120

374 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCCTATTATCTCTGATCCTGATC 433

Db 314 ATGGCTTTGGCCTCAGCTGAGTTGCTGCTGGGAAGAACCTCACTTTCAGAAGA 373

QY 61 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCCTATTATCTCTGATCCTGATC 120

374 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCCTATTATCTCTGATCCTGATC 433

QY 121 TCTGTTGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 180
Db 434 TCTGTTGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 493
QY 181 ATGCCCTCTCGAGGAACACATTCCTTGGGTTTCAGGGATATCTGTAAATGCAACAACCC 240
Db 494 ATGCCCTCTCGAGGAACACATTCCTTGGGTTTCAGGGATATCTGTAAATGCAACAACCC 553
QY 241 TGTTCCTGTTACCGAGCTCTCGGGAGGCTCCGGAGTTTGGGAACATTTAAACAATCC 300
Db 554 TGTTCCTGTTACCGAGCTCTCGGGAGGCTCCGGAGTTTGGGAACATTTAAACAATCC 613
QY 301 ATTGTGGCTCGCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACAC 360
Db 614 ATTGTGGCTCGCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACAC 673
QY 361 AGCATGAAGGACATGGCCAAAGTTCTGAGAACATTAACAGACATCAAGAAATCCAGCTCA 420
Db 674 AGCATGAAGGACATGGCCAAAGTTCTGAGAACATTAACAGACATCAAGAAATCCAGCTCA 733
QY 421 AACTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGGTTCTATATAC 480
Db 734 AACTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGGTTCTATATAC 793
QY 481 AACTCTCTCTCCCAAAGTCTACTGTGGAACAGATGCTGAGGCTGATGTCTATCTCCAC 540
Db 794 AACTCTCTCTCCCAAAGTCTACTGTGGAACAGATGCTGAGGCTGATGTCTATCTCCAC 853
QY 541 AAGTATTTTTCAGGCTACCAAGTTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
Db 854 AAGTATTTTTCAGGCTACCAAGTTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 913
QY 601 GAAGAGATGATTCAACTTGGTGACCAAGAGTTTCTGAGCTTTGTGGCTTCCAAAGGAG 660
Db 914 GAAGAGATGATTCAACTTGGTGACCAAGAGTTTCTGAGCTTTGTGGCTTCCAAAGGAG 973
QY 561 AACTGGCTGCACAGAGGAGTACTGTTGTCACATGGACATGCAATCTGAAGCAATCTCTG 720
Db 974 AACTGGCTGCACAGAGGAGTACTGTTGTCACATGGACATGCAATCTGAAGCAATCTCTG 1033
QY 721 AGAACAATAAATCTACATCTCCCTCCGAGCAAGAGTCTGCTGAAGCCACAAAAACA 780
Db 1034 AGAACAATAAATCTACATCTCCCTCCGAGCAAGAGTCTGCTGAAGCCACAAAAACA 1093
QY 781 TTGCTGCATAGTCTGGGACTCTGGCCAGAGAGTGTTCAGCATGAGAAGCTGGAGTGAC 840
Db 1094 TTGCTGCATAGTCTGGGACTCTGGCCAGAGAGTGTTCAGCATGAGAAGCTGGAGTGAC 1153
QY 841 ATGCGACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 900
Db 1154 ATGCGACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 1213
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Db 1214 TACCAAGCTGTGTCGTAATGTCTGCGGGCATCCGAGGGAGGGGGCTGAAGATCAAG 1273
QY 961 TCTCTCACTGTTATGAGACAAACATACAAAGCCCTCTTTTGGAGGCAATGGCACTGAG 1020
Db 1274 TCTCTCACTGTTATGAGACAAACATACAAAGCCCTCTTTTGGAGGCAATGGCACTGAG 1333
QY 1021 GAAGATGCTGAACCTTCTATGACAACCTCTACAACCTCTTACTGCAATGATTTGATGAAG 1080
Db 1334 GAAGATGCTGAACCTTCTATGACAACCTCTACAACCTCTTACTGCAATGATTTGATGAAG 1393
QY 1081 AATTTGGAGTCTAGTCCCTCTTCCGCAATATCTGGAAGCTCTGAAGCGGTGCTCGTT 1140
Db 1394 AATTTGGAGTCTAGTCCCTCTTCCGCAATATCTGGAAGCTCTGAAGCGGTGCTCGTT 1453
QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAAGGCAAGGCTCATGGCTGAGTGAAAC 1200
Db 1454 GGAAGATCCTGTATACACTGACACTCCAGCCACAAGGCAAGGCTCATGGCTGAGTGAAAC 1513

QY 1201 AAGACCTTCCAGGAACACTGGCTGTGTTCATGATCTGGAAGGCATCTGGAGGAACACTCAGC 1260
Db 1514 AAGACCTTCCAGGAACACTGGCTGTGTTCATGATCTGGAAGGCATCTGGAGGAACACTCAGC 1573
QY 1261 CCCAAGATCTGACCTTCATGAGAACACGCCAAGAAATGGACCTTGTCCGATCTGTTG 1320
Db 1574 CCCAAGATCTGACCTTCATGAGAACACGCCAAGAAATGGACCTTGTCCGATCTGTTG 1633
QY 1321 GACAGCAGGCAATGACACCTTTTGGAAACAGCAGTTGGATGGCTTASATTTGACACGCC 1380
Db 1634 GACAGCAGGCAATGACACCTTTTGGAAACAGCAGTTGGATGGCTTASATTTGACACGCC 1693
QY 1381 CAAGACATCGTGGCCCTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1440
Db 1694 CAAGACATCGTGGCCCTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1753
QY 1441 GTGTACACCTTGAGAGAAAGCTTTTCAACGAGACTTAACAGGCAATCCGGACCATATCTCGC 1500
Db 1754 GTGTACACCTTGAGAGAAAGCTTTTCAACGAGACTTAACAGGCAATCCGGACCATATCTCGC 1813
QY 1501 TTCATGGAGTGTCAACCTGNAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
Db 1814 TTCATGGAGTGTCAACCTGNAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1873
QY 1561 AACAACTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGTATTGTTCACCTGGA 1620
Db 1874 AACAACTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGTATTGTTCACCTGGA 1933
QY 1621 ATTACTCAGGAGCATTTGAGCTGCCCATCATGATCAAGTACAAGATCCGAATGGACATT 1680
Db 1934 ATTACTCAGGAGCATTTGAGCTGCCCATCATGATCAAGTACAAGATCCGAATGGACATT 1993
QY 1681 GACAACTGTGGAGAGGACAAATAAATAAAGATGGGACTGGGACCTGTGCTCTGAGCT 1740
Db 1994 GACAACTGTGGAGAGGACAAATAAATAAAGATGGGACTGGGACCTGTGCTCTGAGCT 2053
QY 1741 GACCCCTTTGAGAGCAATCGGTACGCTCTGGGGGGCTTCGCTACTTTCAGGATGTGGT 1800
Db 2054 GACCCCTTTGAGAGCAATCGGTACGCTCTGGGGGGCTTCGCTACTTTCAGGATGTGGT 2113
QY 1801 GAGCAGGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGGTGTCTATATGCAA 1860
Db 2114 GAGCAGGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGGTGTCTATATGCAA 2173
QY 1861 CAGATGGCCCTATCCCTGTATGATGACATCTTTTCGGGGTGATGAGCCGGTCAATG 1920
Db 2174 CAGATGGCCCTATCCCTGTATGATGACATCTTTTCGGGGTGATGAGCCGGTCAATG 2233
QY 1921 CCCCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGT 1980
Db 2234 CCCCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGT 2293
QY 1981 TATGAGAGGAGGACCGCTGAAAGAGACCATGCGGATCATGCGCCCTGGACACAGCATA 2040
Db 2294 TATGAGAGGAGGACCGCTGAAAGAGACCATGCGGATCATGCGCCCTGGACACAGCATA 2353
QY 2041 CTCCTGGTTTACCTGGTTTCAATAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCTGCTA 2100
Db 2354 CTCCTGGTTTACCTGGTTTCAATAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCTGCTA 2413
QY 2101 GTGTCATCTCTGAAAGTTAGGAAACCTGCTGCCCTACAGTGTATCCAGCTGGTGTGTC 2160
Db 2414 GTGTCATCTCTGAAAGTTAGGAAACCTGCTGCCCTACAGTGTATCCAGCTGGTGTGTC 2473
QY 2161 TTCCTGCTCCGTTTGTGTGGTGACAAATCCTGCAAGTGTCTTCTGATTAAGCACTCTTC 2220
Db 2474 TTCCTGCTCCGTTTGTGTGGTGACAAATCCTGCAAGTGTCTTCTGATTAAGCACTCTTC 2533
QY 2221 TCCAGAGCCAACTGGCAGCAGCTGTGGGGGATCATCTACTTACGGCTGACCTGCC 2280
Db 2534 TCCAGAGCCAACTGGCAGCAGCTGTGGGGGATCATCTACTTACGGCTGACCTGCC 2593
QY 2281 TACGTCCTGTGTGGCATGGCAGGACTACGCTGGGCTTACACTCAAGATCTTTCGCTAGC 2340

Db 2594 TACGCTCTGTGTGGCATGGCAGACACTACGTTGGGCTTACACTCAAGATCTTCGCTAGC 2653
QY 2341 CTGCTGCTCTCCGTGGCTTTTGGGTTTGGCTGTGAGTACTTTTGGCCCTTTTGGAGGACAG 2400
Db 2654 CTGCTGCTCTCCGTGGCTTTTGGGTTTGGCTGTGAGTACTTTTGGCCCTTTTGGAGGACAG 2713
QY 2401 GGCATTGGAGTGCAGTGGGACAACTTTTGGAGTCTCTGTGGAGGAGATGGCTTCAAT 2460
Db 2714 GGCATTGGAGTGCAGTGGGACAACTTTTGGAGTCTCTGTGGAGGAGATGGCTTCAAT 2773
QY 2461 CTCACCACTTCGATCTCCATGATGCTTTGTGACACCTTCCTCTATGGGGTGATGACCTGG 2520
Db 2774 CTCACCACTTCGATCTCCATGATGCTTTGTGACACCTTCCTCTATGGGGTGATGACCTGG 2833
QY 2521 TACATTTAGGCTGTCTTTCCAGGCGAGTACGGAATTCGAGGCCCTTGATTTTCCCTTGC 2580
Db 2834 TACATTTAGGCTGTCTTTCCAGGCGAGTACGGAATTCGAGGCCCTTGATTTTCCCTTGC 2893
QY 2581 ACCAAGTCTACTGTTTGGCAGGAAAGTGTATGAGAGGACCACTGTTTCCCAACACAG 2640
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QY 2641 AAGAGAATCTCAGAAATCTGATGAGGAGGAGAACCCACCTTGAAGCTGGGCGTGTCC 2700
Db 2954 AAGAGAATCTCAGAAATCTGATGAGGAGGAGAACCCACCTTGAAGCTGGGCGTGTCC 3013
QY 2701 ATTCAAGACCTGTAAAGTCTACCGAGATGGTGAAGTGGCTGTGATGGCTGGCA 2760
Db 3014 ATTCAAGACCTGTAAAGTCTACCGAGATGGTGAAGTGGCTGTGATGGCTGGCA 3073
QY 2761 CTGAATTTTTATGAGGGCCAGATCACTCTCTCTGGGCCCAATGAGCGGGGAGAGCG 2820
Db 3074 CTGAATTTTTATGAGGGCCAGATCACTCTCTCTGGGCCCAATGAGCGGGGAGAGCG 3133
QY 2821 ACCACATGTCAATCTGACCGGTTTCCCGCCAGCTCGGGACCGCTACATCCG 2880
Db 3134 ACCACATGTCAATCTGACCGGTTTCCCGCCAGCTCGGGACCGCTACATCCG 3193
QY 2881 GGAAAGACATTCGCTCTGAGATGACACCATCCGCAAGAACTGGGGTCTGTCCCGAG 2940
Db 3194 GGAAAGACATTCGCTCTGAGATGACACCATCCGCAAGAACTGGGGTCTGTCCCGAG 3253
QY 2941 CATACGTGCTGTTTACATGCTGACATGCTGGAAGACACATCTGTTCTATGCCCGCTTG 3000
Db 3254 CATACGTGCTGTTTACATGCTGACATGCTGGAAGACACATCTGTTCTATGCCCGCTTG 3313
QY 3001 AAAGGGCTCTCTGAGAGACAGTGAAGGGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
Db 3314 AAAGGGCTCTCTGAGAGACAGTGAAGGGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3373
QY 3061 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG 3120
Db 3374 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG 3433
QY 3121 CTATCTGTGGCTTGGCTTGTGGGGATCTAAGTTGTCTATCTGGATGAACCCACA 3180
Db 3434 CTATCTGTGGCTTGGCTTGTGGGGATCTAAGTTGTCTATCTGGATGAACCCACA 3493
QY 3181 GCTGGTGTGACCTTTACTCCCGAGGGGAATATGGAGAGTGTGCTGTAATACCGACAA 3240
Db 3494 GCTGGTGTGACCTTTACTCCCGAGGGGAATATGGAGAGTGTGCTGTAATACCGACAA 3553
QY 3241 GGCGGACCAATTTCTCTCTACACACCATGGATGAAGCGGACCTCTGGGGGACAGG 3300
Db 3554 GGCGGACCAATTTCTCTCTACACACCATGGATGAAGCGGACCTCTGGGGGACAGG 3613
QY 3301 ATTGCCATCATCTCCATGGGAAGTGTGCTGTGGGCTCCCTGTTTCTGAAGAAG 3360
Db 3614 ATTGCCATCATCTCCATGGGAAGTGTGCTGTGGGCTCCCTGTTTCTGAAGAAG 3673
QY 3361 CAGCTGGGAACAGCTACTACTCTGACCTTGGTCAAGAAAGATGTGGAATCTCCCTCAGT 3420

Db 3674 CAGCTGGGAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGGAATCTCCCTCAGT 3733
QY 3421 TCCTGCGAARACAGTAGTAGCAGCTGTGTACATCTGAAAGAGGAGACAGTGTTCCTCAG 3480
Db 3734 TCCTGCGAARACAGTAGTAGCAGCTGTGTACATCTGAAAGAGGAGACAGTGTTCCTCAG 3793
QY 3481 AGCAGTTCTGATGCTGGCCTGGCAGGACCATGAGAGTGCACACGCTGACCATCGATGTC 3540
Db 3794 AGCAGTTCTGATGCTGGCCTGGCAGGACCATGAGAGTGCACACGCTGACCATCGATGTC 3853
QY 3541 TCTGCTATCTCCACCTCATCAGGAAGCATGTCTGTAAGCCCGCTGGTGGAGACATA 3600
Db 3854 TCTGCTATCTCCACCTCATCAGGAAGCATGTCTGTAAGCCCGCTGGTGGAGACATA 3913
QY 3601 GGCATGAGCTGACCTATGCTGCTGATGAAGCTGTCTAAGGAGGAGCGCTTGTGGAA 3660
Db 3914 GGCATGAGCTGACCTATGCTGCTGATGAAGCTGTCTAAGGAGGAGCGCTTGTGGAA 3973
QY 3661 CTCCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTCIAGTTATGGCATCTCA 3720
Db 3974 CTCCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTCIAGTTATGGCATCTCA 4033
QY 3721 GAGACGACCTTGGAGAAATATCTCTCAAGTGGCCGAGAGAGTGGGGTGGATGCTGAG 3780
Db 4034 GAGACGACCTTGGAGAAATATCTCTCAAGTGGCCGAGAGAGTGGGGTGGATGCTGAG 4093
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Db 4094 ACCTCAGATGGTACCTTCCAGCAAGACGAGCGGGCTTGGGGCAAGCAGAGC 4153
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Db 4154 TGTCTTCCCGCTTCACTGAGATGATGCTGCTGATCCAAATGATTCAGCATAGACCCA 4213
QY 3901 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGATGTCGCAAGGGTCTTACCAGTGA 3960
Db 4214 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGATGTCGCAAGGGTCTTACCAGTGA 4273
QY 3961 GCTCGAAGCTTACAGACAGACTTGTGGCCCTTTGTGGAGAGACTGCTAATGGC 4020
Db 4274 GCTCGAAGCTTACAGACAGACTTGTGGCCCTTTGTGGAGAGACTGCTAATGGC 4333
QY 4021 AGACGAGTCGGAAGGATTTTGTCTCAGATGCTGTCGCAAGCTGCTGTTCTGCAAT 4080
Db 4334 AGACGAGTCGGAAGGATTTTGTCTCAGATGCTGTCGCAAGCTGCTGTTCTGCAAT 4393
QY 4081 GCTCTGCTTTCAGGCTGATGCTGCCACCTTTGGCAAGTACCAGGCTGGAATCTCAG 4140
Db 4394 GCTCTGCTTTCAGGCTGATGCTGCCACCTTTGGCAAGTACCAGGCTGGAATCTCAG 4453
QY 4141 CCTGAGATGTAACGACAGTACATTTGTGCAATGATGCTCTGAGGACACGGGA 4200
Db 4454 CCTGAGATGTAACGACAGTACATTTGTGCAATGATGCTCTGAGGACACGGGA 4513
QY 4201 ACCCTGGAATCTTTAAACGCTTCAACCAAGACCTTGGCTTCGGGACCGCTGATGGAA 4260
Db 4514 ACCCTGGAATCTTTAAACGCTTCAACCAAGACCTTGGCTTCGGGACCGCTGATGGAA 4573
QY 4261 GGAAACCAATCCAGACAGCGCTTCCAGGAGGAGAGAGTGGACACTGCCCA 4320
Db 4574 GGAAACCAATCCAGACAGCGCTTCCAGGAGGAGAGAGTGGACACTGCCCA 4633
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Db 4634 GTTCCCGACACCATCATGGACCTTCTCCAGAAATGGGAATGCAGAACCTTCA 4693
QY 4381 CTTGATGCTGAGTGTAGAGGACAAAATCAAGAGATGCTGCTGCTGTGTGCTCCAGGG 4440
Db 4694 CTTGATGCTGAGTGTAGAGGACAAAATCAAGAGATGCTGCTGCTGTGTGCTCCAGGG 4753
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Db 4754 GCAGGGGGCTGCTCTCCCAAGAAACAAACACATGCAAGATATCTTCCAGGACCTG 4813

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DB 4814 ACAGGAGAACATTTCCGGATTATCTGGGTGAACACGTATGTGCAGATCATAGCCAAAAGC 4873
QY 4561 TTAAGAACAAAGATCTGGGTGAATGAGTTTAGGTATGGGGCTTTTCCCTGGGTGTCAGT 4620
DB 4874 TTAAGAACAAAGATCTGGGTGAATGAGTTTAGGTATGGGGCTTTTCCCTGGGTGTCAGT 4933
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DB 4934 AATACTCAAGCACTTCTCCGAGTCAAGAGTAAATGATGCCATCAACAAATGAAGAAA 4993
QY 4681 CACCTAAAGCTGGCCAAAGACAGTCTCTGAGATCGATTTCTCAACAGCTTGGGAAGATT 4740
DB 4994 CACCTAAAGCTGGCCAAAGACAGTCTCTGAGATCGATTTCTCAACAGCTTGGGAAGATT 5053
QY 4741 ATGACAGGACTGGACACCAAGAAATAATGTCAAGGTGTGGTTTCAATAACAAAGGCTGGCAT 4800
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DB 5234 CAGCAGCTCTCAGAGTGTCTGTATGACCAATCAGTGGATGCTGTGTGTCATCTGT 5293
QY 4981 GTCATCTTTGCAATGTCCTGTCAGGACGCTTTGCTGATTTCTGATCCAGGAGCGG 5040
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QY 5041 GTCAGAACAAACACCTCGAGTTTCAATGAGTGAAGCCTGTCTACTTACTGGTCT 5100
DB 5354 GTCAGAACAAACACCTCGAGTTTCAATGAGTGAAGCCTGTCTACTTACTGGTCT 5413
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DB 5414 TCTAATTTTGTCTGGATATGTGCAATACGTTGTCTCCAGGACGCTTTGCTGATTTCTATCATC 5473
QY 5161 TTCATCTGTTCCAGAGAGTCTGTATGTCTCCCAATCTGCTGCTGCTAGCCCTT 5220
DB 5474 TTCATCTGTTCCAGAGAGTCTGTATGTCTCCCAATCTGCTGCTGCTAGCCCTT 5533
QY 5221 CTACTTTTGTCTGATGGTCAATCATCCTCTCATGTACCCAGGCTCTCTTGTGTTTC 5280
DB 5534 CTACTTTTGTCTGATGGTCAATCATCCTCTCATGTACCCAGGCTCTCTTGTGTTTC 5593
QY 5281 AAGATCCCAAGACAGCCTATGTGTGCTCACCAGCGTGAACCTCTTCAATGGCATTAAAT 5340
DB 5594 AAGATCCCAAGACAGCCTATGTGTGCTCACCAGCGTGAACCTCTTCAATGGCATTAAAT 5653
QY 5341 GGCAGCGTGGCCACCTTTGCTGTGAGCTGTTCACCGACATAGCTGAATAATATCAAT 5400
DB 5654 GGCAGCGTGGCCACCTTTGCTGTGAGCTGTTCACCGACATAGCTGAATAATATCAAT 5713
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DB 5714 GATATCTGAAGTCCGCTTCTGTATCTTCCACATTTTTCCTGGGACGAGGCTCATC 5773
QY 5461 GACATGGTGAACACCAAGCAATGGCTGATCCCTGGAAGGTTTGGGAGAAATCGTTTT 5520
DB 5774 GACATGGTGAACACCAAGCAATGGCTGATCCCTGGAAGGTTTGGGAGAAATCGTTTT 5833
QY 5521 GTGTACCATTTATCTTGGGACTTGGTGGGAGCAACCTCTTCGCCATGGCGGTGAAGGG 5580
DB 5834 GTGTACCATTTATCTTGGGACTTGGTGGGAGCAACCTCTTCGCCATGGCGGTGAAGGG 5893

QY 5581 GTGGTGTCTTCTCTCATTTACTGTCTGTATCCAGTACAGATCTTCTCATCAGGCCAGACCT 5640
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QY 5641 GTAAATGCAAAAGCTATCTCTCTGATCATGAAGATGAAGATGTGAGCGCGGGAAGACAG 5700
DB 5954 GTAAATGCAAAAGCTATCTCTCTGATCATGAAGATGAAGATGTGAGCGCGGGAAGACAG 6013
QY 5701 AGAATTTCTGTGTGTGGAGCCAGAAATCACATCTTAGAAATCAAGGAGTTGACCAAGATA 5760
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QY 5761 TATAGAAGAGAGGAGGAGCCCTGTGTGTGACAGGATTTGCGTGGGCAATCTCTCTGTGTGAG 5820
DB 6074 TATAGAAGAGAGGAGGAGCCCTGTGTGTGACAGGATTTGCGTGGGCAATCTCTCTGTGTGAG 6133
QY 5821 TGCTTTGGGCTCTCTGGGAGTTAATGGGCTGGAATAATCATCAACTTTCAAGATGTTAAACA 5880
DB 6134 TGCTTTGGGCTCTCTGGGAGTTAATGGGCTGGAATAATCATCAACTTTCAAGATGTTAAACA 6193
QY 5881 GGAGATACCACTGTGTACAGAGGAGATGCTTTTCCCTTAAACAAAATAGTATCTTATCAAAAC 5940
DB 6194 GGAGATACCACTGTGTACAGAGGAGATGCTTTTCCCTTAAACAAAATAGTATCTTATCAAAAC 6253
QY 5941 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
DB 6254 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6313
QY 6001 TTGACTGGGAGAGAACACGTGGAGTTCTTTTCCCTTTTGGAGAGGATCCCCAGAGAAAGAA 6060
DB 6314 TTGACTGGGAGAGAACACGTGGAGTTCTTTTCCCTTTTGGAGAGGATCCCCAGAGAAAGAA 6373
QY 6061 GTTCGCAAGTGTGTGAGTGGGCGATTCGGAACCTGGCCCTCTGTAAGTATGAGAGAAAA 6120
DB 6374 GTTCGCAAGTGTGTGAGTGGGCGATTCGGAACCTGGCCCTCTGTAAGTATGAGAGAAAA 6433
QY 6121 TATCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCATGCTTTGATC 6180
DB 6434 TATCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCATGCTTTGATC 6493
QY 6181 GCGGGGCTCTGTGTGTCTGTGATGACCCACACAGGATGATCCCAAGCCCGG 6240
DB 6494 GCGGGGCTCTGTGTGTCTGTGATGACCCACACAGGATGATCCCAAGCCCGG 6553
QY 6241 CGGTCTCTGTGGAAATGTGCCCTAAGTGTGTCAAGGAGGAGATCAGTAGTGTAC 6300
DB 6554 CGGTCTCTGTGGAAATGTGCCCTAAGTGTGTCAAGGAGGAGATCAGTAGTGTAC 6513
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DB 6614 TCTCATAGTATGGAAGATGTGAAGTCTTTTGCATAGGATGGCAATCATGTCAATGA 6673
QY 6361 AGGTTCAGGTGCTTGGCAGTGTCCAGCATCTAAATAAGTGTGGAGTGTGTTTACA 6420
DB 6674 AGGTTCAGGTGCTTGGCAGTGTCCAGCATCTAAATAAGTGTGGAGTGTGTTTACA 6733
QY 6421 ATAGTTGTAGCAATAGAGGTTCCAAACCCGAGCTGAAAGCCTGCCAGGATTTCTTTTGA 6480
DB 6734 ATAGTTGTAGCAATAGAGGTTCCAAACCCGAGCTGAAAGCCTGCCAGGATTTCTTTTGA 6793
QY 6481 CTTCATTTCTCTGGAAGTGTCTTAAAGAGAAACCCGGAACATGTCTAATACAGCTT 5540
DB 6794 CTTCATTTCTCTGGAAGTGTCTTAAAGAGAAACCCGGAACATGTCTAATACAGCTT 5853
QY 6541 CCATCTTCATTTCTCTTGGCCAGGATATTCAGATCTCTCCAGAGCAAAAAGCA 5600
DB 6854 CCATCTTCATTTCTCTTGGCCAGGATATTCAGATCTCTCCAGAGCAAAAAGCA 6913
QY 6601 CTCACATAGAAAGTACTCTGTCTCTCAGACAACTTGACCAAGTATTTGTGAACCTT 6660
DB 6914 CTCACATAGAAAGTACTCTGTCTCTCAGACAACTTGACCAAGTATTTGTGAACCTT 6973
QY 6661 GCCAAGGACAAAGTGTATGATGACCACTTTAAAGACCTCTCTCATTTACACAAAACAGACA 6720

Accession	Gene	Strain	Sequence
6974	Db	7033	GCACGACCAAGTGATGATGACCACTAAAGACCTCTCATTTACACAAAAACGACACA
6721	Qy	6780	GTAGTGGAGTTGCAGTTCTCACATCTTTCTACAGGATGAGAAGTGAAGAAAGCTAT
7034	Db	7093	GTAGTGGAGCTTGCAGTTCTCACATCTTTCTACAGGATGAGAAGTGAAGAAAGCTAT
6781	Qy	6784	GTAT
7094	Db	7097	GTAT

RESULT 2
US-09-984-827-97
US-09-984-827-97, Application US/09984827
Sequence 97, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEFLÉ, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
METHODS OF DETECTION
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 97
LENGTH: 9870
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (7138)
OTHER INFORMATION: a, t, c or g
US-09-984-827-97

Db	674	AGCATGAAGGACATGCGCCAAAGTTCTTGAGAACATTTACAGCAGATCAAGAAATTCAGCTCA	733
Qy	421	AAC TTGAAGCTTCAAGATTTCC TTGGTGAGCAATGAACCTTCTCTGGGTTCTATATCAC	480
Db	734	AAC TTGAAGCTTCAAGATTTCC TTGGTGAGCAATGAACCTTCTCTGGGTTCTGTATCAC	793
Qy	481	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCTATCTCCAC	540
Db	794	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCTATCTCCAC	853
Qy	541	AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	600
Db	854	AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	913
Qy	601	GAAGAGATGATTCAAC TTGGTGACCAAGAAGTTTCTGAC TTTGTGGCTACCAAGGAG	660
Db	914	GAAGAGATGATTCAAC TTGGTGACCAAGAAGTTTCTGAC TTTGTGGCTACCAAGGAG	973
Qy	661	AAAC TGGCTGCAGACAGACGAGTACTTCGTTTCCAACTGGACATCCTGAAGCCAATCTGT	720
Db	974	AAAC TGGCTGCAGACAGACGAGTACTTCGTTTCCAACTGGACATCCTGAAGCCAATCTGT	1033
Qy	721	AGAACACTAAACTCTACATCTCCCTTCCCGAAGCAGAGCTGGCTGAGCCCAAAAACA	780
Db	1034	AGAACACTAAACTCTACATCTCCCTTCCCGAAGCAGAGCTGGCTGAGCCCAAAAACA	1093
Qy	781	TTGCTGCATGATCTTGGACCTCTGGCCACGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	840
Db	1094	TTGCTGCATGATCTTGGACCTCTGGCCACGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	1153
Qy	841	ATCCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC	900
Db	1154	ATCCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC	1213
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Db	1214	TACGAGGCTGTCTCGTATTGTTCTGGGGCATCCCGAGGGAGGGGGCTGAGATCAAG	1273
Qy	961	TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020
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Qy	1021	GAAGATGCTGAACCTTCTATGAACAATCTACAACTCCTTACTGCAATGATTTGATGAAG	1080
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Qy	1081	AATTTGGAGCTAGTCCCTTTCCGGCATATCTGGAAGCTCTGAAGCGCTGCTCGTT	1140
Db	1394	AATTTGGAGCTAGTCCCTTTCCGGCATATCTGGAAGCTCTGAAGCGCTGCTCGTT	1453
Qy	1141	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGCAGGTCTATGGCTGAGGTGAAC	1200
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Qy	1201	AAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGAAGGCATGTTGGGAGGAACTCAGC	1260
Db	1514	AAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGAAGGCATGTTGGGAGGAACTCAGC	1573
Qy	1261	CCCAAGATCTGGACCTTCATGTGAGAACACCCAGAAGATGGACCTTGTCGGATGCTGTTG	1320
Db	1574	CCCAAGATCTGGACCTTCATGTGAGAACACCCAGAAGATGGACCTTGTCGGATGCTGTTG	1633
Qy	1321	GACAGAGGACATGACACACTTTTGGAAACAGCAGTTGGATGCTTAGATTGGACAGCC	1380
Db	1634	GACAGAGGACATGACACACTTTTGGAAACAGCAGTTGGATGCTTAGATTGGACAGCC	1693
Qy	1381	CACAGACATCTGGCGTTTTTGGCCAAAGCACCCAGAGGATGCCAGTCCAGTAAATGGTTCT	1440
Db	1694	CACAGACATCTGGCGTTTTTGGCCAAAGCACCCAGAGGATGCCAGTCCAGTAAATGGTTCT	1753
Qy	1441	GTGTACACCTTGGAGAGAAGCTTTCACAGAGACTAACACAGGCAATCCCGACCATATCTCGC	1500
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Db 1874 AACAAAGTCCATGGAGCTGTGGATGAGAGGAAGTTCCTGGCTGGTATGTGTTCACTGGA 1933
QY 1621 ATTACTCCAGGCACATGAGCTGCCCATCATGCTCAAGTACAGATCCCAATGGACATT 1680
Db 1934 ATTACTCCAGGCACATGAGCTGCCCATCATGCTCAAGTACAGATCCCAATGGACATT 1993
QY 1681 GACAATGTGAGAGGCAAAATAAAATCAAGGATGGGTACTGGACCCCTGGTCTCGAGCT 1740
Db 1994 GACAATGTGAGAGGCAAAATAAAATCAAGGATGGGTACTGGACCCCTGGTCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATCGCGTACGTCTGGGGGCTTCGCCCTACTTTGAGGATGGTG 1800
Db 2054 GACCCCTTTGAGGACATCGCGTACGTCTGGGGGCTTCGCCCTACTTTGAGGATGGTG 2113
QY 1801 GAGCAGCAATCATCAGGTTGCTGAGGGCACCAGAGAGAAACTGGTGTATATGCAA 1860
Db 2114 GAGCAGCAATCATCAGGTTGCTGAGGGCACCAGAGAGAAACTGGTGTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTACGTGTGATGACATCTTTCTCGGGTGATGACCGGTCAATG 1920
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QY 1921 CCCTCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980
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QY 1981 TATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTGACACACAGATA 2040
Db 2294 TATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTGACACACAGATA 2353
QY 2041 CTCTGGTTTACGTTGTTCAATAGTACCTTACTTCTTCTTCTGAGCGCTGGCTGCTA 2100
Db 2354 CTCTGGTTTACGTTGTTCAATAGTACCTTACTTCTTCTTCTGAGCGCTGGCTGCTA 2413
QY 2101 GTGGTCACTCTGAAGTTAGAAACCTGTGCCCTACAGTATCCAGCGTGTGTTGTC 2160
Db 2414 GTGGTCACTCTGAAGTTAGAAACCTGTGCCCTACAGTATCCAGCGTGTGTTGTC 2473
QY 2161 TTCCTGTCCGTGTTTCTGTGTGACATCTTCCAGTGTCTTCTATAGCACATCTTC 2220
Db 2474 TTCCTGTCCGTGTTTCTGTGTGACATCTTCCAGTGTCTTCTATAGCACATCTTC 2533
QY 2221 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTTACCTGCTGTACCTGCC 2280
Db 2534 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTTACCTGCTGTACCTGCC 2593
QY 2281 TAGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTCGCTAGC 2340
Db 2594 TAGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTCGCTAGC 2653
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 Db 6254 ATCCATGAAGTACATCAGACATGGCTACTGCGCTCAGTTTATGCCATCAGAGAGCTG 6313
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RESULT 3
 US-09-984-827-101
 ; Sequence 101, Application US/09984827
 ; Publication No. US2003005623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEUFLE, PATRICE
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
 ; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984,827
 ; CURRENT FILING DATE: 2002-04-01
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 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 101
 ; LENGTH: 9870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (7138)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-101

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
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 Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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3134 ACCACCATGTCAATCTCTGACCGGTTTCTCCCGCCAGCTCGGGCCACCGCTACATCTCTG 3193
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DB 3914 GGGCATGAGCTGACCTATGCTGCTGATGAGCTGTAAGGAGGAGGACCTTTGTGAA 3973
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DB 3974 CTCCTTATGAGATGATGACCGGCTCTCAGACCTGGCATTTCTAGTTATGGCATCTCA 4033
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DB 4034 GAGAGACCTTGGAGAAATATTCCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 4093
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QY 4021 AGACGGAGTCGGAAGGATTTTTTGTCTCAGATGTTCTTTGCCAGTGTGTTTGTCTGCA 4080
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DB 4574 GGAACCCCAATCCACAGACACGCTTCCAGGAGGAGGAGAGTGGACACTGCCCA 4633
QY 4321 GTTCCCGAGACATCATGAGCTCTTTCAGAAATGGAACTGGAAATGCAGAACCTTCA 4380
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DB 4754 GCAGGGGGCTGCTCTCCACAAAGAAACAAACACTGCAGATATCTTTCAGGACCTG 4813
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Db 6254 ATCCATGAAGTACATCAGACATGGGCTACTGCTCCCTCAGTTGATGCCATCAGAGCTG 6313
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QY 6061 GTTGGCAAGGTTGTGAGTGGGCGATTGCGAACTGGGCACTGTAAGATATGGAGAAAA 6120
Db 6374 GTTGGCAAGGTTGTGAGTGGGCGATTGCGAACTGGGCACTGTAAGATATGGAGAAAA 6433
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QY 6781 GTAT 6784
Db 7094 GTAT 7097

RESULT 4

US-09-984-827-103
; Sequence 103, Application us/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENESELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USBS, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-103

Query Match          99.7%; Score 6766.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGTGATC 120
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DB 434 TCTGTTGGCTGAGCTACCCACCTATGACACATGAATGCCATTTTCCAAATAAGCC 493
QY 181 ATGGCTTGTGGCTCAGCTGAGTTCCTGCTGTGGAAGAACCTCACTTTTCAGAAAGA 240
DB 494 ATGGCTTGTGGCTCAGCTGAGTTCCTGCTGTGGAAGAACCTCACTTTTCAGAAAGA 553
QY 241 TGTTCGGTTACCGAGCTCCTGGGAGGCTCCGGAGTGTGGAACATTTTAAACAATCC 300
DB 554 TGTTCGGTTACCGAGCTCCTGGGAGGCTCCGGAGTGTGGAACATTTTAAACAATCC 613
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DB 614 ATTTGGCTCCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACCC 673
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DB 794 AACTCTCTCCCAAGTCTACTGTGGAAGATGCTGAGGCTGATCTCATTCCTCAC 853
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QY 901 TACCAGGCTGTGCTCTATTTGTGCGGCAATCCCGAGGAGGGGGGTGAAGATCAAG 960
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DB 1814 TTCTAGGAGTGTCTCAACCTGAACAGCTAGAACCCTAGACACAGAACTCTGGCTCATC 1873
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DB 2114 GAGCAGCAATCATCAGGGTCTGAGGGGACCGAGAAAGAACTGCTCTATATGCA 2173
QY 1861 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGCTGATGAGCCGGTCAATG 1920
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QY 1921 CCCCTCTTCATGAGCTGCGCTGCTGATTTACTAGTGGCTGATCATCAAGGCAATCGTG 1980
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QY 2041 CTCCTGTTTAGCTGGTTCAATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGCTGCTA 2100

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Db	2414		GTGGTCATCCTCAAGTAGGAAACCTGCTGCCCTACAGTCATCCACGCTGGTGTGGTC	2473
Qy	2161		TTGCTGTCCGCTGTTTGGTGAGCAATCCTGCAGTGCCTTCTGATTAGCACACTCTTC	2220
Db	2474		TTCTGTCCGCTGTTTGGTGAGCAATCCTGCAGTGCCTTCTGATTAGCACACTCTTC	2533
Qy	2221		TCAGAGCCAACTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTAACCTGCC	2280
Db	2534		TCAGAGCCAACTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTAACCTGCC	2593
Qy	2281		TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACATCAAGATCTTCGCTAGC	2340
Db	2594		TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACATCAAGATCTTCGCTAGC	2653
Qy	2341		CTGCTGTCCTCTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG	2400
Db	2654		CTGCTGTCCTCTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG	2713
Qy	2401		GGCATGGAGTGCAGTGGCAGCAACCTGTTTGAGAGTCTCTGTGAGGAAGATGCTTCAAT	2460
Db	2714		GGCATGGAGTGCAGTGGCAGCAACCTGTTTGAGAGTCTCTGTGAGGAAGATGCTTCAAT	2773
Qy	2461		CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGTGATGACCTGG	2520
Db	2774		CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGTGATGACCTGG	2833
Qy	2521		TACATTGAGCTGCTCTTCCAGCGCAGTACGGAATCCAGGGCCCTGGTATTTTCCTTGG	2580
Db	2834		TACATTGAGCTGCTCTTCCAGCGCAGTACGGAATCCAGGGCCCTGGTATTTTCCTTGG	2893
Qy	2581		ACCAAGTCCTACTGGTTTGGGAGGAAAGTGTAGAGAGAGCCACCTGGTTCACACCAAG	2640
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Qy	2641		AAGAGATGTCAGAAATCTGCATGGAGGAGGAACCCACCACTTGAAGCTGGCGGTGTC	2700
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Qy	2701		ATTCAGAACCTTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCCTGGCA	2760
Db	3014		ATTCAGAACCTTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCCTGGCA	3073
Qy	2761		CTGAATTTTTATGAGGCCAGATCACCCTCTCTCTGGCGGCACATGAGCGGGGAGAGCG	2820
Db	3074		CTGAATTTTTATGAGGCCAGATCACCCTCTCTCTGGCGGCACATGAGCGGGGAGAGCG	3133
Qy	2821		ACCACCATGTCAATCTGTACCGGGTGTTCGCCCGGACCTGGGCAACGCTACATCCTG	2880
Db	3134		ACCACCATGTCAATCTGTACCGGGTGTTCGCCCGGACCTGGGCAACGCTACATCCTG	3193
Qy	2881		GGAAAGACATTCGCTCTGAGATGAGCACCATTCGCGGCACATGAGCGGGGAGAGCG	2940
Db	3194		GGAAAGACATTCGCTCTGAGATGAGCACCATTCGCGGCACATGAGCGGGGAGAGCG	3253
Qy	2941		CATACGTCGCTGTTTGACATGCTGACTGTCGAGAAACACATCTGTTCTATGCGCCGCTTG	3000
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Qy	3001		AAAGGGCTCTCTGAGAGCAGCTGAAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3060
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Qy	3061		TTGCCATCAACGAGCTGAAGACCAAAACAGCCAGCTGTCAGGTGGAAATCACAGAAAG	3120
Db	3374		TTGCCATCAACGAGCTGAAGACCAAAACAGCCAGCTGTCAGGTGGAAATCACAGAAAG	3433
Qy	3121		CTATCTGTGGCTTGGCTTTGTGGGGGATCTTAAGGTTGTCAATCTGATGAACCCACA	3180

Db	3434	CTATCTGFGCCCTTTGTGGGGGATCTTAAAGTTGTCTANTCTGGATGAACCCACA	3439
Qy	3181	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAATAACGACAA	3240
Db	3494	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAATAACGACAA	3553
Qy	3241	GGCCGACCATATATCTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG	3300
Db	3554	GGCCGACCATATATCTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG	3613
Qy	3301	ATTGGCATCATCTCCCATGGGAAGCTGTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3360
Db	3614	ATTGGCATCATCTCCCATGGGAAGCTGTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3673
Qy	3361	CAGCTGGGAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGGATTCCTCCTCAGT	3420
Db	3674	CAGCTGGGAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGGATTCCTCCTCAGT	3733
Qy	3421	TCCTGCAGAAACAGTAAAGCACTGTGTACCTGTCAACCTGAAAAAGGAGACAGTGTTCCTCAG	3488
Db	3734	TCCTGCAGAAACAGTAAAGCACTGTGTACCTGTCAACCTGAAAAAGGAGACAGTGTTCCTCAG	3793
Qy	3481	AGCAGTTCTGATGTGGGCTTGGGACGACCAATGAGATGACACCTGACCATCATGTC	3540
Db	3794	AGCAGTTCTGATGTGGGCTTGGGACGACCAATGAGATGACACCTGACCATCATGTC	3853
Qy	3541	TCGTCTATCTCCAACTCATCAGGAAGCATGTCTGAAGCCCGCTGGTGGAAACACATA	3600
Db	3854	TCGTCTATCTCCAACTCATCAGGAAGCATGTCTGAAGCCCGCTGGTGGAAACACATA	3913
Qy	3601	GGGCATGAGCTGACCTATGTGTCGCATATGAAGTGTCTAAGGAGGGAGCCCTTTGTGGAA	3660
Db	3914	GGGCATGAGCTGACCTATGTGTCGCATATGAAGTGTCTAAGGAGGGAGCCCTTTGTGGAA	3973
Qy	3661	CNCTTTTCATGATTCAGCCGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA	3720
Db	3974	CNCTTTTCATGATTCAGCCGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA	4033
Qy	3721	GAGACACCCCTGGAAGAAATATTCCTCAAGTGGCCGGAAGAGAGTGGGTGGATGCTGAG	3780
Db	4034	GAGACACCCCTGGAAGAAATATTCCTCAAGTGGCCGGAAGAGAGTGGGTGGATGCTGAG	4093
Qy	3781	ACCTCAGATGGTACCTTGCACGACGACCAACAGCGCGGCTTCGGGACACAGCAGAC	3840
Db	4094	ACCTCAGATGGTACCTTGCACGACGACCAACAGCGCGGCTTCGGGACACAGCAGAC	4153
Qy	3841	TGTCTTCGCCGCTTCACTGAAAGATGATGCTGTGATCCAAATGATTCGACATAGACCCA	3900
Db	4154	TGTCTTCGCCGCTTCACTGAAAGATGATGCTGTGATCCAAATGATTCGACATAGACCCA	4213
Qy	3901	GAATCAGAGACAGACATTTGCTGAGATGGATGGCAAGGGTCCCTACCAGGTGAAC	3960
Db	4214	GAATCAGAGACAGACATTTGCTGAGATGGATGGCAAGGGTCCCTACCAGGTGAAC	4273
Qy	3961	GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGAAGAGAGATGCTTAATTGCC	4020
Db	4274	GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGAAGAGAGATGCTTAATTGCC	4333
Qy	4021	AGACGGAGTCGGAAGAGATTTTTTGTCTCAGATGTCTTGCCAGCTGTGTTGTCTGCATT	4080
Db	4334	AGACGGAGTCGGAAGAGATTTTTTGTCTCAGATGTCTTGCCAGCTGTGTTGTCTGCATT	4393
Qy	4081	GCCTTTGTCTCAGCTGATCGTGCCACCTTTGGCAAGTACCCACGCTGGAACTTCAG	4140
Db	4394	GCCTTTGTCTCAGCTGATCGTGCCACCTTTGGCAAGTACCCACGCTGGAACTTCAG	4453
Qy	4141	CCCTGGATGTACAACGAAACAGTACATTTTGTGAGCAATGATGCTCCTGAGGACACGGGA	4200
Db	4454	CCCTGGATGTACAACGAAACAGTACATTTTGTGAGCAATGATGCTCCTGAGGACACGGGA	4513
Qy	4201	ACCCCTGAACTCTTAAACGCCCTTACCAAAGACCTGGCTTCGGGACCCGCTGTATGGAA	4260
Db	4514	ACCCCTGAACTCTTAAACGCCCTTACCAAAGACCTGGCTTCGGGACCCGCTGTATGGAA	4573

QY	5341	GGCAGCTGGCCACCTTTTGCTGGAGCTGTCTCACGGACAAATAACTGATATATCAAT	5400
DB	5654	GGCAGCTGGCCACCTTTTGCTGGAGCTGTCTCACGGACAAATAACTGATATATCAAT	5713
QY	5401	CATATCTGAAGTCGCGTGTCTTTGATCTTCCACATTTTGCCTGGGACGAGGGCTCATC	5460
DB	5714	GATATCTGAAGTCGCGTGTCTTTGATCTTCCACATTTTGCCTGGGACGAGGGCTCATC	5773
QY	5461	GACATGGTGAAAAACACAGGCAATGGCTGATGCCCTGGAAAGTTTCTGGGAGATCGCTTT	5520
DB	5774	GACATGGTGAAAAACACAGGCAATGGCTGATGCCCTGGAAAGTTTCTGGGAGATCGCTTT	5833
QY	5521	GTGTCAACCATATCTTTGGGACTTTGGTGGGACGAACACTCTTCGCCATGGCCGTGGAAGGG	5580
DB	5834	GTGTCAACCATATCTTTGGGACTTTGGTGGGACGAACACTCTTCGCCATGGCCGTGGAAGGG	5893
QY	5581	GTGTGTGTCTTCTTCATTACTGTCTTGATGTCAGTACAGATTCTTCATCAGGCCACAGACCT	5640
DB	5894	GTGTGTGTCTTCTTCATTACTGTCTTGATGTCAGTACAGATTCTTCATCAGGCCACAGACCT	5953
QY	5641	GTAATCAAAAGCTATCTCCTCTCAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
DB	5954	GTAATCAAAAGCTATCTCCTCTCAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	6013
QY	5701	AGAAATTCCTGATGGTGGAGGCCAGAAATGACATCTTAGAAATCAAGGAGTTGACGNAGATA	5760
DB	6014	AGAAATTCCTGATGGTGGAGGCCAGAAATGACATCTTAGAAATCAAGGAGTTGACGNAGATA	6073
QY	5761	TATAGAAGGAAGCGGAAGCCCTGCTGTGACAGGATTCGGTGGGATTCCTCCTCGGTGAG	5820
DB	6074	TATAGAAGGAAGCGGAAGCCCTGCTGTGACAGGATTCGGTGGGATTCCTCCTCGGTGAG	6133
QY	5821	TGCTTTGGCTCTCTGGAGTTATGGGCTGGAAATCATCACTTTCAGATGCTTAACTACA	5880
DB	6134	TGCTTTGGCTCTCTGGAGTTATGGGCTGGAAATCATCACTTTCAGATGCTTAACTACA	6193
QY	5881	GGAGATACCACTGTTACAGAGGAGATGCTTTCCTTAAACAAAATAGTATCTTATCAAC	5940
DB	6194	GGAGATACCACTGTTACAGAGGAGATGCTTTCCTTAAACAGAATAGTATCTTATCAAC	6253
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTCATGCCATCACAGAGCTG	6000
DB	6254	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTCATGCCATCACAGAGCTG	6313
QY	6001	TTGACTGGGAGAACACACGTGGAGTTCTTTTGCCCTTTTGAGAGGAGTCCAGAGAAAGAA	6060
DB	6314	TTGACTGGGAGAACACACGTGGAGTTCTTTTGCCCTTTTGAGAGGAGTCCAGAGAAAGAA	6373
QY	6061	GTTGGCAAGTGTGTGTAGTGGGCGATTGCGAACTGGGCTCGTCAAGTATGTGGAGAAAA	6120
DB	6374	GTTGGCAAGTGTGTGTAGTGGGCGATTGCGAACTGGGCTCGTCAAGTATGTGGAGAAAA	6433
QY	6121	TATGCTGGTAACTATAGTGGAGGCAACAACCGCAGCTCTCTACAGCCATGGCTTGTATC	6180
DB	6434	TATGCTGGTAACTATAGTGGAGGCAACAACCGCAGCTCTCTACAGCCATGGCTTGTATC	6493
QY	6181	GGCGGGCTCCTGTGGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6240
DB	6494	GGCGGGCTCCTGTGGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6553
QY	6241	CGGTTCTTGTGGAATTTGTGCCCTTAAGTGTGTTCAGGAGGGGAGATCAGTATGCTTACA	6300
DB	6554	CGGTTCTTGTGGAATTTGTGCCCTTAAGTGTGTTCAGGAGGGGAGATCAGTATGCTTACA	6613
QY	6301	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAATGGA	6360
DB	6614	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAATGGA	6673
QY	6361	AGGTTCAAGTGGCTTGGCAGTGTGCCAGATCTTAAAAATAGGTTTGGAGATGGTTATACA	6420
DB	6674	AGGTTCAAGTGGCTTGGCAGTGTGCCAGATCTTAAAAATAGGTTTGGAGATGGTTATACA	6733
QY	6421	ATAGTTGTACGAATAGCAGGGTCCAAACCCGGACCTGAAGCCCTGTCCAGGATTTCTTTGGA	6480

Db 6734 ATAGTGTACGATAGAGGTCCTCAACCGGACCTGGAAGCTGTCCAGGATTTCTTIGGA 6793
QY 6481 CTTGCAATTCCTGGAGTGTCTTAAAGAGAAACACCGGACATGCTACATACCACTT 6540
Db 6794 CTTGCAATTCCTGGAGTGTCTTAAAGAGAAACACCGGACATGCTACATACCACTT 6853
QY 6541 CCATCTTCAATATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6600
Db 6854 CCATCTTCAATATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6913
QY 6601 CTCACATAGAGACTACTCTCTCTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6660
Db 6914 CTCACATAGAGACTACTCTCTCTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6973
QY 6661 GCGAAGGACCAAGTATGATGACACACITAAAGACCTCTCATACCAAAAACCAAGACA 6720
Db 6974 GCGAAGGACCAAGTATGATGACACACITAAAGACCTCTCATACCAAAAACCAAGACA 7033
QY 6721 GTAGTGGAGCTTGCAGTCTCTCATCTCTCTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7034 GTAGTGGAGCTTGCAGTCTCTCATCTCTCTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7093
QY 6781 GTAT 6784
Db 7094 GTAT 7097

RESULT 5

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; Sequence 105, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUINE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
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; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c o r g
US-09-984-827-105

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGCTTGTGGCTCAGCTGAGTGTGCTGCTGTGGAAGAACCTCACTTTTCAGAAAGA 60
Db 314 ATGCTTGTGGCTCAGCTGAGTGTGCTGCTGTGGAAGAACCTCACTTTTCAGAAAGA 373
QY 61 CAAACATGTCAGCTGTGCTGGAAGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 120
Db 374 CAAACATGTCAGCTGTGCTGGAAGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 433
QY 121 TCTGTCGGCTGAGCTACCCACCTATGACACATGAATGCCATTTTCCAAATAAGCC 180

Db 434 TCTGTCGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAGCC 493
QY 181 ATGCCCTCTCAGGAACACATCTCTTGGTTCAGGGGATATCTCTAATGCAACAACCC 240
Db 494 ATGCCCTCTCAGGAACACATCTCTTGGTTCAGGGGATATCTCTAATGCAACAACCC 553
QY 241 TGTTCCTGTACCCTGACTCCTGGGAGGCTCCCGAGGTGTGTGAAAATTTTAAACAATCC 300
Db 554 TGTTCCTGTACCCTGACTCCTGGGAGGCTCCCGAGGTGTGTGAAAATTTTAAACAATCC 613
QY 301 ATTTGGCTCCCTGCTCTCAGATGCTCGGAGGCTCTCTTTTATACAGCCAGAAAGACCC 360
Db 614 ATTTGGCTCCCTGCTCTCAGATGCTCGGAGGCTCTCTTTTATACAGCCAGAAAGACCC 673
QY 361 AGCATGAAGGACATCGCAAAAGTTCTGTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 420
Db 674 AGCATGAAGGACATCGCAAAAGTTCTGTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 733
QY 421 AACTTGAAGCTTCAAGATTTCTGTGTGACAAATGAAACCTTCTCTGSGTTCCTATATCAC 480
Db 734 AACTTGAAGCTTCAAGATTTCTGTGTGACAAATGAAACCTTCTCTGSGTTCCTATATCAC 793
QY 481 AACCTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGGTGATGTCTCATTTCCAC 540
Db 794 AACCTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGGTGATGTCTCATTTCCAC 853
QY 541 AAGGTATTTTGGCAAGGCTACAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 600
Db 854 AAGGTATTTTGGCAAGGCTACAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 913
QY 601 GAAGAGATGATTCAACTTGGTGACCAAGAGTTTCTGTAGCTTTGTGGCTTACCAAGGAG 660
Db 914 GAAGAGATGATTCAACTTGGTGACCAAGAGTTTCTGTAGCTTTGTGGCTTACCAAGGAG 973
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Db 974 AAACCTGGCTGACGAGCGAGTACTCTGTTCCAAACATGGACATCCTGAAGCAATCTCTG 1033
QY 721 AGAACACTAAACTCTACATCTCCCTCCCGACAGAGGCTGGCTGAGCCCAAAAACA 780
Db 1034 AGAACACTAAACTCTACATCTCCCTCCCGACAGAGGCTGGCTGAGCCCAAAAACA 1093
QY 781 TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAAC 840
Db 1094 TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAAC 1153
QY 841 ATGCGACAGGAGGTGATGTTTCTGACCAATGTGACAGCTCCAGCTCCCTCCCAAAATC 900
Db 1154 ATGCGACAGGAGGTGATGTTTCTGACCAATGTGACAGCTCCAGCTCCCTCCCAAAATC 1213
QY 901 TACCAGGCTGTGTCTCGTATTGTCTGCGGCTATCCCGAGGAGGGGCTGAAGATCAAG 960
Db 1214 TACCAGGCTGTGTCTCGTATTGTCTGCGGCTATCCCGAGGAGGGGCTGAAGATCAAG 1273
QY 961 TCTCTCACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
Db 1274 TCTCTCACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1333
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTTGATGAAG 1080
Db 1334 GAAGATGCTGAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTTGATGAAG 1393
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QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAGCAGCTCATGCTGAGGTGAAC 1200
Db 1454 GGAAGATCCTGTATACACTGACACTCCAGCCACAGCAGCTCATGCTGAGGTGAAC 1513
QY 1201 AAGACCTTCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCTGTGGAGGAACCTCAGC 1260
Db 1514 AAGACCTTCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCTGTGGAGGAACCTCAGC 1573

QY 1261 CCCAAGATCTGGACCTTCATATGGAGAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTG 1320
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QY 1321 GACAGCAGGACATGACCACTTTTGGACACAGCTTGGATGGCTTAGATGGACAGCC 1380
Db 1634 GACAGCAGGACATGACCACTTTTGGACACAGCTTGGATGGCTTAGATGGACAGCC 1693
QY 1381 CAAGACATCGTGGCGTTTGGCCAAAGCACCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1440
Db 1694 CAAGACATCGTGGCGTTTGGCCAAAGCACCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1753
QY 1441 GTGTACACCTGGAGAGAGCTTTCACGAGACTAACACAGCAATCCGGACCATATCTCGC 1500
Db 1754 GTGTACACCTGGAGAGAGCTTTCACGAGACTAACACAGCAATCCGGACCATATCTCGC 1813
QY 1501 TTCAATGGAGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGCTCTGGCTCATC 1560
Db 1814 TTCAATGGAGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGCTCTGGCTCATC 1873
QY 1561 AACAAAGTCCATGAGAGCTGCTGGATGAGAGAGTTCCTGGCGTGGTATGTTCTACTGGA 1620
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QY 1621 ATTACTCCAGGACAGCATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1680
Db 1934 ATTACTCCAGGACAGCATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1993
QY 1681 GACAAATGGAGAGACAAATAAATCAAGATGGGTACTGGACCCCTGGTCTCTGAGCT 1740
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QY 1741 GACCCCTTTGAGACATGGGTACGCTCTGGGGGCTTCGCTACTTCAGAGATGGTG 1800
Db 2054 GACCCCTTTGAGACATGGGTACGCTCTGGGGGCTTCGCTACTTCAGAGATGGTG 2113
QY 1801 GAGCAGGCAATCATAGGCTGTGACGGCCACCGAGAGAAACCTGGTCTATATGCAA 1860
Db 2114 GAGCAGGCAATCATAGGCTGTGACGGCCACCGAGAGAAACCTGGTCTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTACCTTGTATGACATCTTCTGCGGGTATGACCGGTCATG 1920
Db 2174 CAGATGCCCTATCCCTGTACCTTGTATGACATCTTCTGCGGGTATGACCGGTCATG 2233
QY 1921 CCCCCTTTCAATGACCTGGCCCTGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 1980
Db 2234 CCCCCTTTCAATGACCTGGCCCTGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 2293
QY 1981 TATGAGAGGAGGACGCTGAAAGAGACCATGCGGATCATTGGGCTGGACAAAGCATA 2040
Db 2294 TATGAGAGGAGGACGCTGAAAGAGACCATGCGGATCATTGGGCTGGACAAAGCATA 2353
QY 2041 CTCCTGGTTAGCTGGTTCATTAGTAGTACCTTCTCTCTTGTGAGCGCTGGCTGCTA 2100
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QY 2101 GTGGTCATCCCTGAAATAGGAACCTGTGCCCTACAGTAGATCCAGCGTGGTGTGTC 2160
Db 2414 GTGGTCATCCCTGAAATAGGAACCTGTGCCCTACAGTAGATCCAGCGTGGTGTGTC 2473
QY 2161 TTCCTGTCCGTGTTGCTGTGGTGAATCTGACATCTGACGTCTCTCCGATAGCACACTCTC 2220
Db 2474 TTCCTGTCCGTGTTGCTGTGGTGAATCTGACATCTGACGTCTCTCCGATAGCACACTCTC 2533
QY 2221 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTACTTACGCTGTACTCGCC 2280
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Db 2594 TAGCTTCTGTGTGGCATGGCAGACTAGTGGGCTTCACACTCAAGATCTTCGCTAGC 2653

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QY 2461 CTCACCACTTCCATCTCCATGATGCTGTTTGGACACTTCTCTCTATGGGATGATGACCTGG 2520
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QY 2761 CTGAATTTTATGAGGCGCAGATCACCTTCTCTGGGCCACATGAGGCGGGAAGACG 2820
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QY 3361 CAGCTGGGAACAGGCTACTACCTGACCTTGGTGAAGAAAGATGTGGAATCTCCCTCAGT 3420
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Db 3734 TCCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAGAGGACAGAGTGTCTCAG 3793
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 QY 3901 GAATCAGAGACAGACATTTGCTCAGTGGATGGATGGCAAGGGTCTTACCAGGTGMAA 3960
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 QY 3961 GGTGTGAACCTTACAGCAACAGTGTGTGGCCCTTTTGTGGAAGAGCTGCTAAATGGC 4020
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 Db 4514 ACCCTGGAACCTTTAAAGCCCTCACCAGACCCCTGGCTTGGGACCCGCTGTATGGA 4573
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RESULT 6
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Deneffe, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: FOJO, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
; FILE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent version 3.0
; SEQ ID NO 10
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

Query Match          99.7%; Score 6764.8; DB 10; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTCTGATCCCTGATC 120
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QY 181 ATGCCCTCTGCAGAAACACITTCCTTGGTTCAGGGGATTAATCTGTAATGCCAACACCCC 240
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QY 241 TGTTCCTGTTACCCGACTCCTCGGGAGGCTCCCGGAGTTGTTGGAACITTTAAACAATCC 300
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QY 301 ATGTCGCTGCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACACC 360
DB 485 ATGTCGCTGCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACACC 544
QY 361 AGCATGAAGGACATGCCAAAGTCTCAGAAACATTACAGCAGATCAAGAAATCCAGCTCA 420
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QY 4441 GCAGGGGGCTGCTCTCCACAAAGAAAACAACTCAGATATCCCTTCAGGACCTG 4500
Db 4625 GCAGGGGGCTGCTCTCCACAAAGAAAACAACTCAGATATCCCTTCAGGACCTG 4684
QY 4501 ACAGGAAGAAACATTTCCGATTAATCTGGTGAAGACGATGTCAGATCATAGCCAAAGC 4560
Db 4685 ACAGGAAGAAACATTTCCGATTAATCTGGTGAAGACGATGTCAGATCATAGCCAAAGC 4744
QY 4561 TTAAGAAACAGATCTGGTGAATGAGTTTAGGTATGGCGCTTTCCCTGGGTGTCAGT 4620
Db 4745 TTAAGAAACAGATCTGGTGAATGAGTTTAGGTATGGCGCTTTCCCTGGGTGTCAGT 4804
QY 4621 AATACTCAAGCATTTCTCCAGTCAAGAGTTAATGATGCCATCAAAACAAATGAAGAA 4680
Db 4805 AATACTCAAGCATTTCTCCAGTCAAGAGTTAATGATGCCATCAAAACAAATGAAGAA 4864
QY 4681 CACTAAGCTGCCAGGACGATTTCTGAGATCGATTTCTCAACAGCTTGGAGATTT 4740
Db 4865 CACTAAGCTGCCAGGACGATTTCTGAGATCGATTTCTCAACAGCTTGGAGATTT 4924
QY 4741 ATGACAGGACTGGACACCCAGAAATAATGTCAAGGCTGTGTTCAATAACAGGCTGGCAT 4800
Db 4925 ATGACAGGACTGGACACCCAGAAATAATGTCAAGGCTGTGTTCAATAACAGGCTGGCAT 4984

QY	4801	GC	AATCAGCTCTTTCTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGC	CAAAAG	4861	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG
QY	4802	GC	AATCAGCTCTTTCTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGC	CAAAAG	4862	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG
DB	4985	GC	AATCAGCTCTTTCTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGC	CAAAAG	5044	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG
QY	4861	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG	4920	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG
DB	5045	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG	5104	GG	AGAAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCTGAAATCTC	CACCAAG
QY	4921	CAC	GAGCTCTCAGAGGTGGCTCTGATGACACACATCAGTGGAGTCCCTTGTGTCAT	CTGTT	4980	CAC	GAGCTCTCAGAGGTGGCTCTGATGACACACATCAGTGGAGTCCCTTGTGTCAT	CTGTT
DB	5105	CAC	GAGCTCTCAGAGGTGGCTCCGATGACCAATCAGTGGAGTCCCTTGTGTCAT	CTGTT	5164	CAC	GAGCTCTCAGAGGTGGCTCCGATGACCAATCAGTGGAGTCCCTTGTGTCAT	CTGTT
QY	4981	GT	CATCTTTTGC	AATGTCCTCCAGCCAGCTTTGCTGATTCCTGATCCAGAGCGG	5040	GT	CATCTTTTGC	AATGTCCTCCAGCCAGCTTTGCTGATTCCTGATCCAGAGCGG
DB	5165	GT	CATCTTTTGC	AATGTCCTCCAGCCAGCTTTGCTGATTCCTGATTCCTGATTC	5224	GT	CATCTTTTGC	AATGTCCTCCAGCCAGCTTTGCTGATTCCTGATTCCTGATTC
QY	5041	GT	CACAAAGCAAAACACCTGCAGTTCATCAGTGAGTGAAGCGTGCATCTACT	TG	5100	GT	CACAAAGCAAAACACCTGCAGTTCATCAGTGAGTGAAGCGTGCATCTACT	TG
DB	5225	GT	CACAAAGCAAAACACCTGCAGTTCATCAGTGAGTGAAGCGTGCATCTACT	TG	5284	GT	CACAAAGCAAAACACCTGCAGTTCATCAGTGAGTGAAGCGTGCATCTACT	TG
QY	5101	TC	TAAATTTTGTCTGGGATGTGCAATACGTTTGCCCTGCCACACTGGTCATTAT	CATC	5160	TC	TAAATTTTGTCTGGGATGTGCAATACGTTTGCCCTGCCACACTGGTCATTAT	CATC
DB	5285	TC	TAAATTTTGTCTGGGATGTGCAATACGTTTGCCCTGCCACACTGGTCATTAT	CATC	5344	TC	TAAATTTTGTCTGGGATGTGCAATACGTTTGCCCTGCCACACTGGTCATTAT	CATC
QY	5161	TT	CATCTGCTTCACAGCAGAAGTCCTATGTGTCTCCACCAATTCGCTGTGCTAG	CCGCTT	5220	TT	CATCTGCTTCACAGCAGAAGTCCTATGTGTCTCCACCAATTCGCTGTGCTAG	CCGCTT
DB	5345	TT	CATCTGCTTCACAGCAGAAGTCCTATGTGTCTCCACCAATTCGCTGTGCTAG	CCGCTT	5404	TT	CATCTGCTTCACAGCAGAAGTCCTATGTGTCTCCACCAATTCGCTGTGCTAG	CCGCTT
QY	5221	CT	ACTTTTGTGTTATGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTT	TGTGTT	5280	CT	ACTTTTGTGTTATGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTT	TGTGTT
DB	5405	CT	ACTTTTGTGTTATGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTT	TGTGTT	5464	CT	ACTTTTGTGTTATGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTT	TGTGTT
QY	5281	AA	GATCCCCAGACACGCTATGTGTGCTCCACGCGTGAACCTCTTCATTGGCATTA	TAAT	5340	AA	GATCCCCAGACACGCTATGTGTGCTCCACGCGTGAACCTCTTCATTGGCATTA	TAAT
DB	5465	AA	GATCCCCAGACACGCTATGTGTGCTCCACGCGTGAACCTCTTCATTGGCATTA	TAAT	5524	AA	GATCCCCAGACACGCTATGTGTGCTCCACGCGTGAACCTCTTCATTGGCATTA	TAAT
QY	5341	GG	CAGGTGGCCACCTTTGTGTGGAGCTGTTCACCGACAATAAGCTGAATAATAT	CAAT	5400	GG	CAGGTGGCCACCTTTGTGTGGAGCTGTTCACCGACAATAAGCTGAATAATAT	CAAT
DB	5525	GG	CAGGTGGCCACCTTTGTGTGGAGCTGTTCACCGACAATAAGCTGAATAATAT	CAAT	5584	GG	CAGGTGGCCACCTTTGTGTGGAGCTGTTCACCGACAATAAGCTGAATAATAT	CAAT
QY	5401	GA	TATCTCTGAAGTCGCTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGCT	CATC	5460	GA	TATCTCTGAAGTCGCTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGCT	CATC
DB	5585	GA	TATCTCTGAAGTCGCTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGCT	CATC	5644	GA	TATCTCTGAAGTCGCTGTTCTTGATCTTCCACATTTTTGCCTGGGACGAGGCT	CATC
QY	5461	GAC	ATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAA	TCTGTTT	5520	GAC	ATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAA	TCTGTTT
DB	5645	GAC	ATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAA	TCTGTTT	5704	GAC	ATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAA	TCTGTTT
QY	5521	GT	GTCACCAATATCTTTGGACCTTGTGGGACGAAACCTCTTCGCCATGGCCG	TGGAGGG	5580	GT	GTCACCAATATCTTTGGACCTTGTGGGACGAAACCTCTTCGCCATGGCCG	TGGAGGG
DB	5705	GT	GTCACCAATATCTTTGGACCTTGTGGGACGAAACCTCTTCGCCATGGCCG	TGGAGGG	5764	GT	GTCACCAATATCTTTGGACCTTGTGGGACGAAACCTCTTCGCCATGGCCG	TGGAGGG
QY	5581	GT	GCTGTCTCTCCTCATTAATCTGTCTGATCCAGTACAGATCTTTCATCAGGC	CCAGACCT	5640	GT	GCTGTCTCTCCTCATTAATCTGTCTGATCCAGTACAGATCTTTCATCAGGC	CCAGACCT
DB	5765	GT	GCTGTCTCTCCTCATTAATCTGTCTGATCCAGTACAGATCTTTCATCAGGC	CCAGACCT	5824	GT	GCTGTCTCTCCTCATTAATCTGTCTGATCCAGTACAGATCTTTCATCAGGC	CCAGACCT
QY	5641	GTA	AATGCAAAAGTATCTCCTCTGAATGATGAAGATGAAGTGTGAGCGGGAA	AAGACAG	5700	GTA	AATGCAAAAGTATCTCCTCTGAATGATGAAGATGAAGTGTGAGCGGGAA	AAGACAG
DB	5825	GTA	AATGCAAAAGTATCTCCTCTGAATGATGAAGATGAAGTGTGAGCGGGAA	AAGACAG	5884	GTA	AATGCAAAAGTATCTCCTCTGAATGATGAAGATGAAGTGTGAGCGGGAA	AAGACAG
QY	5701	AGA	ATCTTCTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCAC	CAAGATA	5760	AGA	ATCTTCTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCAC	CAAGATA
DB	5885	AGA	ATCTTCTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCAC	CAAGATA	5944	AGA	ATCTTCTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCAC	CAAGATA
QY	5761	TAT	AGAGGAGCGGAGGCTGCTGTTGACAGGATTTGCGTGGGATTCCTCTCTG	TGTGAG	5820	TAT	AGAGGAGCGGAGGCTGCTGTTGACAGGATTTGCGTGGGATTCCTCTCTG	TGTGAG
DB	5945	TAT	AGAGGAGCGGAGGCTGCTG					

Db	6065	GGAGTACCAGCTGTTACAGAGGAGATGCTTTCCCTTACAGAAATAGTAICTTATCAAC	6124
Qy	5941	ATCCATGAAGTACATCAGAACATGGGCTACTCCCTCAGTTTGATGCCATCACAGCTG	6000
Db	6125	ATCCATGAAGTACATCAGAACATGGGCTACTCCCTCAGTTTGATGCCATCACAGAGCTG	6184
Qy	6001	TTGACTGGGAGAACACGCTGGAGTCTTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6060
Db	6185	TTGACTGGGAGAGAACACGCTGGAGTCTTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6244
Qy	6061	GTTGGCAAGTTGGTGAGTGGCGGATTCGGAAACTGGGCCCTCGTAGATATGGAGAAAA	6120
Db	6245	GTTGGCAAGTTGGTGAGTGGCGGATTCGGAAACTGGGCCCTCGTAGATATGGAGAAAA	6304
Qy	6121	TATCGTGAATATAGTGGAGCAACAACGCAAGCTCTCTACAGCCATGCGTTTGATC	6180
Db	6305	TATCGTGAATATAGTGGAGCAACAACGCAAGCTCTCTACAGCCATGCGTTTGATC	6364
Qy	6181	GGCGGGCCTCCTGTGGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCGG	6240
Db	6365	GGCGGGCCTCCTGTGGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCGG	6424
Qy	6241	CGGTTCTGTGGAAATCTGCGCCCTAACTGTTGTCAGGAGGGAGATCACTAGTCTTACA	6300
Db	6425	CGGTTCTGTGGAAATCTGCGCCCTAACTGTTGTCAGGAGGGAGATCACTAGTCTTACA	6484
Qy	6301	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACCTAGATGGCAATCATGGTCAATGGA	6360
Db	6485	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACCTAGATGGCAATCATGGTCAATGGA	6544
Qy	6361	AGGTTTCAGTGCCCTTGGCAGTGCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6420
Db	6545	AGGTTTCAGTGCCCTTGGCAGTGCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6604
Qy	6421	ATAGTTGTACGAATAGCAGGGTCCACCCCGACCTGGAAGCCTGTCCAGGATTTCTTTGGA	6480
Db	6605	ATAGTTGTACGAATAGCAGGGTCCACCCCGACCTGGAAGCCTGTCCAGGATTTCTTTGGA	6664
Qy	6481	CTTCGATTTCTGGAAGTGTTCTAAAGAGAAACACCGGAACATGCTCAATATCCAGCTT	6540
Db	6665	CTTCGATTTCTGGAAGTGTTCTAAAGAGAAACACCGGAACATGCTCAATATCCAGCTT	6724
Qy	6541	CCATCTTCATATCTCTCGGCCAGGATATTCAGATCCTCTCCAGAGCAAAAGCGA	6600
Db	6725	CCATCTTCATATCTCTCGGCCAGGATATTCAGATCCTCTCCAGAGCAAAAGCGA	6784
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Qy	6661	GCCAAGGACCAAGTGATGATGACCACTTAAAGAGCCTCTATTACAAAAACGAGACA	6720
Db	6845	GCCAAGGACCAAGTGATGATGACCACTTAAAGAGCCTCTATTACAAAAACGAGACA	6904
Qy	6721	GTATGGAGCTTGCAGTTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	6780
Db	6905	GTATGGAGCTTGCAGTTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	6964
Qy	6781	GTAT 6784	
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RESULT 7
US -03-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOUD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS

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: APPLICANT: CAMBIEN, FRANCOIS
: TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
: TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
: FILE REFERENCE: 03806.0522-00000
: CURRENT APPLICATION NUMBER: US/09/984,827
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 60/254,108
: PRIOR FILING DATE: 2000-12-11
: PRIOR APPLICATION NUMBER: FR 00/14037
: PRIOR FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 92
: LENGTH: 9870
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: modified_base
: LOCATION: (7138)
: OTHER INFORMATION: a, t, c or g
US-09-984-827-92

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Query Match          99.7%; Score 6764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY	1	ATGGCTTGTTGGCCTCAGCTGAGTTGCTGCTGGAGAACCCTCACTTTCAGAGAAGA	60
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QY	61	CAAAACATGTCAGCTGTTACTTGAAGTGGCCTGGCCTCTATTTATCTTCTGATCCTGATC	120
Db	374	CAAAACATGTCAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCTGATCCTGATC	433
QY	121	TCGTGTTGGCTGAGCTACCCACCCTATGAACAAACATGAATGCGATTTTCCAAATAAAGCC	180
Db	434	TCGTGTTGGCTGAGCTACCCACCCTATGAACAAACATGAATGCGATTTTCCAAATAAAGCC	493
QY	181	ATGCCCTCTGCAGGAACACTTCTCTGGGTTCAGGGATATCTGTAATGCCAACAAACCC	240
Db	494	ATGCCCTCTGCAGGAACACTTCTCTGGGTTCAGGGATATCTGTAATGCCAACAAACCC	553
QY	241	TGTTTCGGTTACCGGACTCCTCGGAGGCTCCGGAGTGTGGAAACTTTTAAACAATCC	300
Db	554	TGTTTCGGTTACCGGACTCCTCGGAGGCTCCGGAGTGTGGAAACTTTTAAACAATCC	613
QY	301	ATTGTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTATACAGCCAGAAAGACACC	360
Db	614	ATTGTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTATACAGCCAGAAAGACACC	673
QY	361	AGCATGAAGGACATGGCGAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGGTCA	420
Db	674	AGCATGAAGGACATGGCGAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGGTCA	733
QY	421	AACCTGAAAGCTCAAGATTTCTCGTGGNACATGAACCTTCTCTGGGTTCCTATATCAC	480
Db	734	AACCTGAAAGCTCAAGATTTCTCGTGGNACATGAACCTTCTCTGGGTTCCTATATCAC	793
QY	481	AACCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGTGTGATGTCATTCTCCAC	540
Db	794	AACCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGTGTGATGTCATTCTCCAC	853
QY	541	AAGGTATTTTTGCAAGGCTACCAAGTTACATTGACAAGTCGTGCAATGGATCAAAATCA	600
Db	854	AAGGTATTTTTGCAAGGCTACCAAGTTACATTGACAAGTCGTGCAATGGATCAAAATCA	913
QY	601	GAAGGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTACCAAAGGAG	660
Db	914	GAAGGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTACCAAAGGAG	973
QY	661	AAACTGGCTGCAGCAGAGGAGTACTTCGTTCCAACTGAGACATCCCTGAAGCCAAATCCTG	720
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QY 1081 AATTGGAGTCTAGTCTCTTTCCCGCATATCTGGAAGCCTGGAAGCGGCTGCTCGTT 1140
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QY 1621 ATTACTCCAGGAGGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1934 ATTACTCCAGGAGGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1993
QY 1681 GACAAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT 1740
Db 1994 GACAAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATGGGTGCTGCTGGGGGCTTGGGCTTACTTCCAGGATGTTGGT 1800
Db 2054 GACCCCTTTGAGGACATGGGTGCTGCTGGGGGCTTGGGCTTACTTCCAGGATGTTGGT 2113
QY 1801 GAGCAGGAATCATCAGGCTGCTGACGGGACCCAGAGAAAGAACTGGTGTCTATATGCAA 1860
Db 2114 GAGCAGGAATCATCAGGCTGCTGACGGGACCCAGAGAAAGAACTGGTGTCTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTTAGTTGATGACATCTTTTCGGGGTGTATGAGCGGTCAATG 1920
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QY 1921 CCCCTTCTCATGACCTGGCTGGATTTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 1980
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Db 2354 CTCCTGTTTACTGTTTATTAGTAGCTCATCTCTCTTCTTGTGAGCGTGGCTGCTGCTA 2413

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QY 2701 ATTCAAGCCTGTGTAAGTCTACCGAGATGGGATGAAGTGGCTGTGCGATGCGCTGGCA 2760
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QY 5701 AGAATTTCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACGAGATA 5760
Db 6014 AGAATTTCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACGAGATA 6073
QY 5761 TATAGAAGAAAGGGAAGCCTGCTGTTGACAGGATTTGGGTGGGATTCCTCTCGTGAG 5820
Db 6074 TATAGAAGAAAGGGAAGCCTGCTGTTGACAGGATTTGGGTGGGATTCCTCTCGTGAG 6133
QY 5821 TGTCTTGGGCTCTCTGGAGTTAATGGGCTGGAATATCAACTTTCAAGATGTTAACA 5880
Db 6134 TGTCTTGGGCTCTCTGGAGTTAATGGGCTGGAATATCAACTTTCAAGATGTTAACA 6193
QY 5881 GGAGTACCACCTGTTACAGAGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 5940
Db 6194 GGAGTACCACCTGTTACAGAGAGATGCTTCTTAAACAAAATAGTATCTTATCAAC 6253
QY 5941 ATCCATGAAGTATACATCAGAACATGGCTACTGCCCTCAGTTTGTGATGCCATCAGAGTG 6000
Db 6254 ATCCATGAAGTATACATCAGAACATGGCTACTGCCCTCAGTTTGTGATGCCATCAGAGTG 6313
QY 6001 TTGACTGGGAGAGACACCTGGAGTTCTTTGGCTTTTGGAGGAGTCCAGAGAAAGAA 6060
Db 6314 TTGACTGGGAGAGACACCTGGAGTTCTTTGGCTTTTGGAGGAGTCCAGAGAAAGAA 6373
QY 6061 GTTGGCAAGTTGGTGGAGTGGCGATCGGAACCTGGGCTCGTGAAGTATGGAAGAAA 6120
Db 6374 GTTGGCAAGTTGGTGGAGTGGCGATCGGAACCTGGGCTCGTGAAGTATGGAAGAAA 6433
QY 6121 TATGCTGTAACATATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGCTTTGATC 6180
Db 6434 TATGCTGTAACATATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGCTTTGATC 6493
QY 6181 GCGGGCCCTCTGCTGCTGTTCTGGATGAACCCACAGCATGATCCCAAGCCCGG 6240
Db 6494 GCGGGCCCTCTGCTGCTGTTCTGGATGAACCCACAGCATGATCCCAAGCCCGG 6553
QY 6241 CGGTTCTTGTGAATTTGCCCTTAAGTGTGTCAGAGGAGGAGATCAGTAGTGTATACA 6300
Db 6554 CGGTTCTTGTGAATTTGCCCTTAAGTGTGTCAGAGGAGGAGATCAGTAGTGTATACA 6613
QY 6301 TCTCATAGTATGGAAGATGTAAGCTCTTTCACATAGATGGCAATCATGTCAATGGA 6360
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QY 6361 AGGTTCCAGTGGCTTGGCAGTGTCCAGATCTAAAAATAGTTTTGGAGATGTTTATACA 6420
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QY 6421 ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGATTTCTTTGGA 6480
Db 6734 ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGATTTCTTTTGA 6793

QY 6481 CTTGCAATTTCTGGAAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACAGCTT 6540
Db 6794 CTTGCAATTTCTGGAAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACAGCTT 6853
QY 6541 CCACTCTCATTTATCTTCTGCGCCAGGATATTCAGCATTCCTCTCCAGAGCAAAAGCGA 6600
Db 6854 CCACTCTCATTTATCTTCTGCGCCAGGATATTCAGCATTCCTCTCCAGAGCAAAAGCGA 6913
QY 6601 CTCACATAGAAAGACTACTCTGTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT 6660
Db 6914 CTCACATAGAAAGACTACTCTGTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT 6973
QY 6661 GCCAAGACCACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 6720
Db 6974 GCCAAGACCACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 7033
QY 6721 GTAGTGGACGTTGAGTCTCAGATCTTCTACAGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7034 GTAGTGGACGTTGAGTCTCAGATCTTCTACAGATGAGAAAGTGAAGAAAGCTAT 7093
QY 6781 GAT 6784
Db 7094 GAT 7097

RESULT 9

US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-94

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGCTTGTGGCCCTCAGCTGAGGTTGCTGCTGTGGAGAACCTCACTTTTCAGAGAGA 60
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QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCCTGCTCTATTATCTTCCTGATCCTGATC 120
Db 374 CAACATGTCAGCTGCTGCTGGAAGTGGCCTGCTCTATTATCTTCCTGATCCTGATC 433
QY 121 TCTGTTGGCTGAGCTACCCACCTCATGACACATGAATGCCATTTTCCAAATAAGGC 180
Db 434 TCTGTTGGCTGAGCTACCCACCTCATGACACATGAATGCCATTTTCCAAATAAGGC 493

QY 181 ATGCCCTCTGCAGAACACTCTCTTGGGTTACGGGATATCTGTAATGCCAACACCC 240
 Db 494 ATGCCCTCTGCAGAACACTCTCTTGGGTTACGGGATATCTGTAATGCCAACACCC 553
 QY 241 TGTTCGGTTACCGACTCTCTGGGAGGCTCCGGAGTTGTTGGAACTTTACAAATCC 300
 Db 554 TGTTCGGTTACCGACTCTCTGGGAGGCTCCGGAGTTGTTGGAACTTTACAAATCC 613
 QY 301 ATTGTGGCTCGCCTGTTCTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACCC 360
 Db 614 ATTGTGGCTCGCCTGTTCTCAGATGCTCGAGGCTCTTTTATACAGCCAGAAAGACCC 673
 QY 361 AGCATGAAGGACATCGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 420
 Db 674 AGCATGAAGGACATCGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 733
 QY 421 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAAACCTTCTTGGGTTCTATATAC 480
 Db 734 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAAACCTTCTTGGGTTCTATATAC 793
 QY 481 AAGCTCTCTCTCCAAAGTCTACTGTGGACAAAGTCTGAGGCTGATGTCATTTCCAC 540
 Db 794 AAGCTCTCTCTCCAAAGTCTACTGTGGACAAAGTCTGAGGCTGATGTCATTTCCAC 853
 QY 541 AAGTATTTTCAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
 Db 854 AAGTATTTTCAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 913
 QY 601 GAAGAGATGATCAACTTGGTGACCAAGAGTTTCTGAGCTTGTGGCTTACCAAGAG 660
 Db 914 GAAGAGATGATCAACTTGGTGACCAAGAGTTTCTGAGCTTGTGGCTTACCAAGAG 973
 QY 661 AAATGGCTGACAGAGGAGTACTTCTGTCACATGGACATCTGAAAGCAATCTCTG 720
 Db 974 AAATGGCTGACAGAGGAGTACTTCTGTCACATGGACATCTGAAAGCAATCTCTG 1033
 QY 721 AGAACACTAACTCTACATCTCCCTTCCCGAGCAAGGAGTGGCTGAAGCCCAAAATCA 780
 Db 1034 AGAACACTAACTCTACATCTCCCTTCCCGAGCAAGGAGTGGCTGAAGCCCAAAATCA 1093
 QY 781 TTGCTGCATAGTCTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAACTGGAGTAC 840
 Db 1094 TTGCTGCATAGTCTGGGACTCTGGCCAGGAGCTGTTTCAGCATGAGAACTGGAGTAC 1153
 QY 841 ATGCGACAGAGGTGATGTTTCTGACCAATGTGAACAGTCCAGCTCCCTCCACCCAAATC 900
 Db 1154 ATGCGACAGAGGTGATGTTTCTGACCAATGTGAACAGTCCAGCTCCCTCCACCCAAATC 1213
 QY 901 TACCAGGCTGTCTCGTATTTCTGCGGCAATCCCGAGGAGGGGGGCTGAAGATCAAG 960
 Db 1214 TACCAGGCTGTCTCGTATTTCTGCGGCAATCCCGAGGAGGGGGGCTGAAGATCAAG 1273
 QY 961 TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGSCACTGAG 1020
 Db 1274 TCTCTCAACTGGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGSCACTGAG 1333
 QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTGATGAG 1080
 Db 1334 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTGATGAG 1393
 QY 1081 AATTGGAGTCTAGTCTCTTTCCCGCATTTACTGGAAGCTCTGAAAGCCGCTGCTGTT 1140
 Db 1394 AATTGGAGTCTAGTCTCTTTCCCGCATTTACTGGAAGCTCTGAAAGCCGCTGCTGTT 1453
 QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCCAAGGAGGTCATGGCTGAGGTGAAC 1200
 Db 1454 GGAAGATCCTGTATACACTGACACTCCAGCCCAAGGAGGTCATGGCTGAGGTGAAC 1513
 QY 1201 AGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGATGTGGAGGAAGTCAAG 1260
 Db 1514 AGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGATGTGGAGGAAGTCAAG 1573
 QY 1261 CCCAAGATCTGACCTTCATGAGAACACCAAGAAATGAGACCTTGTCCGGATGCTGTTG 1320

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 QY 1321 GACAGAGGACATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTTGACAGCC 1380
 Db 1634 GACAGAGGACATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTTGACAGCC 1693
 QY 1381 CAAGACATCTGTGGCTTTTGGCCAAAGCAGGAGTGTCCAGTCCAGTAATGGTTCT 1440
 Db 1694 CAAGACATCTGTGGCTTTTGGCCAAAGCAGGAGTGTCCAGTCCAGTAATGGTTCT 1753
 QY 1441 GTGTACACTGGAGAGAAGCTTTCAACGAGACTTAACAGGCAATCCGGACCATATCTCGC 1500
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 QY 1621 ATTACTCCAGCAGCATGAGCTGCCCATCATGTCAGATACAGATCCGAATCGACAT 1680
 Db 1934 ATTACTCCAGCAGCATGAGCTGCCCATCATGTCAGATACAGATCCGAATCGACAT 1993
 QY 1681 GACAACTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT 1740
 Db 1994 GACAACTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT 2053
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 Db 2054 GACCCCTTTGAGGACATCGGTACGCTCTGGGGGGCTTGGCTTACTTCCAGGATGGTG 2113
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 Db 2114 GAGCAGGCAATCATCAGGCTGCTGACGGGACCCAGAGAAAGAACTGGTGTCTATATGCA 2173
 QY 1861 CAGATGCCCTATCCCTGTTTACGTTGATGACATCTTTCTGCGGGTGTAGCGCGGTCAATG 1920
 Db 2174 CAGATGCCCTATCCCTGTTTACGTTGATGACATCTTTCTGCGGGTGTAGCGCGGTCAATG 2233
 QY 1921 CCCCCTTTTACGCTGCTGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGATCGTG 1980
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Qy 2701 ATTCAAGACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCTGSCA 2760
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Db 3134 ACCACATGTCATCTGACCGGGTGTTCGCCCGACCTCGGGCACCGCTACATCCTG 3193
Qy 2881 GGAAGAACATTCGCTCTGAGATGAGCACCATTCGGCGAGAACCTTGGGGTCTGTCGCCAG 2940
Db 3194 GGAAGAACATTCGCTCTGAGATGAGCACCATTCGGCGAGAACCTTGGGGTCTGTCGCCAG 3253
Qy 2941 CATACAGTCTGTTGACATGCTGACTCTGAAGAACACATCTGTTCTATGCCGCTTG 3000
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Qy 3001 AAAGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
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Qy 3241 GSCCGCACCATTTCTCTACACACACATGGATGAAGCGGAGCTCTGGGGGACAGG 3300
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Db 3614 ATTGCCATCATCTCCATGGGAAGTGTGCTGTGTGGCTCTCTCCCTGTTTCTGAAGAAC 3673
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Db 4274 GGTCTGAACTTACACAGCAACAGTGTGTGGCCCTTTTGTGGAAGAGACTGTCTGCTGCT 4333
Qy 4021 AGCGGAGTCTGGAAGGATTTTGTCTCAGATGCTGTGCGACGCTGTGTTGCTGCTGCT 4080
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Qy 4321 GTTCCCCAGACCATCATGAGACCTCTTCCAGATGGGAACCTGGACAATGCAAGAACCTTCA 4380
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Qy 4381 CTTGATGCGCAGTGTAGCAGCGCAAAATCAAGAAAGTGTGCTGCTGTGCTCCCCAGGG 4440
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Qy 4501 ACAGGAAGAACATTTGCGATTATCTGGTGAAGACGATGTGTCAGATCATAGCCAAAGC 4560
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Db 7034 GTAGTGACGTTGCAGTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 7093

QY 6781 GTAT 6784

Db 7094 GTAT 7097

RESULT 10

US-09-984-827-115
 ; Sequence 115, Application US/09984827
 ; Publication No. US20030056234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEFELE, PATRICE
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984,827
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/254,108
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: FR 00/14037
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 115

; LENGTH: 9870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (7138)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-115

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGCTTGTGGCCTCAGCTGAGTGTGCTGTGGAAGAACTCCTCCTTTCAGAAAGA 60
 Db 314 ATGGCTTGTGGCCTCAGCTGAGTGTGCTGTGGAAGAACTCCTCCTTTCAGAAAGA 373
 QY 61 CAAACATGTCAGCTGTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCTGATC 120
 Db 374 CAAACATGTCAGCTGTGGAAGTGGCTGGCTCTATTATCTTCTGATCTGATC 433
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 Db 434 TCTGTTGGCTGAGCTACCCCTATGAAACATGATGCAATTTTCCAAATAAGGCC 493
 QY 181 ATGCCCTGTCAGGAACTTCTTGGTTCAGGGATATCTGTAAGCCCAACACCCC 240
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 Db 554 TGTTCCTGTTACCCGACTCTCTGGGAGGCTCCCGAGTGTGTGAAACTTTTAAACAATCC 613
 QY 301 ATGTGGCTGCGCTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCCAAGACACC 360
 Db 614 ATGTGGCTGCGCTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCCAAGACACC 673
 QY 361 AGCATGAAGGACATCGCAAAAGTCTTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 420
 Db 674 AGCATGAAGGACATCGCAAAAGTCTTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 733
 QY 421 AACTTGAAGCTCAAGATTTCTGTTGACAAATGAACCTTCTCTGGTTCCTATATCAC 480
 Db 734 AACTTGAAGCTTCAAGATTTCTGTTGACAAATGAACCTTCTCTGGTTCCTATATCAC 793

QY 481 AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTATCTCCAC 540
 Db 794 AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTATCTCCAC 853
 QY 541 AAGGTATTTTTCGAAGGCTACCAAGTTACATTTTACAAAGTCTGTGCAATGGATCAAAATCA 600
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 QY 721 AGAACACTAAACTTACATCTCCCTTCCGAGCAAGGAGTGGCTGAGCCCAACAAACA 780
 Db 1034 AGAACACTAAACTTACATCTCCCTTCCGAGCAAGGAGTGGCTGAGCCCAACAAACA 1093
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RESULT 11

US-09-984-827-119

; Sequence 119, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFFLE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; TITLE OF INVENTION: DETECTION-METHODS AND KITS THEREFOR

FILE REFERENCE: 03806.0523-00000

CURRENT APPLICATION NUMBER: US/09/984,827

CURRENT FILING DATE: 2002-04-01

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PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/14037

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 119

LENGTH: 9870

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: modified_base

LOCATION: (7138)

OTHER INFORMATION: a, t, c or g

US-09-984-827-119

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 2821 ACCACCATGTCAATCTCTGACCGGTTTCCCGCCAGCTCGGGCAGCCGCTACATCTCTG 2880
Db 3134 ACCACCATGTCAATCTCTGACCGGTTTCCCGCCAGCTCGGGCAGCCGCTACATCTCTG 3193
Qy 2881 GGAAGAGACATCTGCTCTGATGATGAGCACCATCGGGCAGAACCTGGGGTCTGTCCCCAG 2940
Db 3194 GGAAGAGACATCTGCTCTGATGATGAGCACCATCGGGCAGAACCTGGGGTCTGTCCCCAG 3253

QY 2941 CATAACGTGCTGTGTGACATGCTGACGTGCGAAGAACACATCTGGTTCATGCCCCCTTG 3000
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QY 5101 TCTAATTTTGTCTGGGATGTGCAATTTACGTTGTGCCCTGCCACACTGGTCTATTATC 5160
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QY 5461 GACATGGTGAACCAACAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCGCTTT 5520
Db 5774 GACATGGTGAACCAACAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCGCTTT 5833
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QY 6001 TTGACTGGGAGAGACACCTGGAGTCTTTGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6060
Db 6314 TTGACTGGGAGAGACACCTGGAGTCTTTGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6373
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Db 6374 GTTGGCAAGTTTGGTGAAGTGGCGGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAA 6433
QY 6121 TATGCTGTTAATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
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Db 6614 TCTCATAGTATGGAAGAAATGTAAGCTCTTTGCACACTAGGATGGCAATCATGGTCAATGGA 6673
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Db 7094 GTAT 7097

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; APPLICANT: DENEFFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
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Query Match									
Best Local Similarity 99.7%; Score 6764.8; DB 9; Length 9870;									
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;									
QY	1	ATGGCTGTGTGGCTCAGCTGAGTGTGCTGTGGAAGAACTCTCACTTTCAGAGAAGA	60						
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Db	374	CAAAATGTCAGCTGTACTGGAAGTGGCTGGCCCTATTATCTCTGATCTCTGATC	433						
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Db	434	TCGTGTCGGCTAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCC	493						
QY	181	ATGCCCTCTGCAGAACACTCTCTGGGTTCAGGGGATATCTGTATGCCACACACCC	240						
Db	494	ATGCCCTCTGCAGAACACTCTCTGGGTTCAGGGGATATCTGTATGCCACACACCC	553						
QY	241	TGTTTCGGTACCCGACTCCTGGGAGGCTCCCGAGTGTGGAACTTTTAAACAATCC	300						
Db	554	TGTTTCGGTACCCGACTCCTGGGAGGCTCCCGAGTGTGGAACTTTTAAACAATCC	613						
QY	301	ATTGTGGCTGGCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCAGAAAGACCC	360						
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QY	361	AGCATGAAGACATCGCGAAAGTCTGAGAACATTTACAGACATCAAGAAATCCAGCTCA	420						
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QY	481	AACTCTCTCTCCAAAGTCTACTGTGGACAGATGCTCAGGGCTGATGTCATCTCCAC	540						
Db	794	AACTCTCTCTCCAAAGTCTACTGTGGACAGATGCTCAGGGCTGATGTCATCTCCAC	853						
QY	541	AAGGTATTTTGAAGGCTACCAAGTTCATTTGACAAAGTCTGTGCAATGGATCAAAATCA	600						
Db	854	AAGGTATTTTGAAGGCTACCAAGTTCATTTGACAAAGTCTGTGCAATGGATCAAAATCA	913						
QY	601	GAAGATGATTAACCTTGGTGACCAAGAGTTCTCGAGCTTGTGGCCCTACCAAGGAG	660						
Db	914	GAAGATGATTAACCTTGGTGACCAAGAGTTCTCGAGCTTGTGGCCCTACCAAGGAG	973						
QY	661	AAACTGGCTGCAGCAGCAGTACTTCTGTTCCAAATGGACATCTGAAAGCCAAATCCCTG	720						
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QY	721	AGAACCTAACTCTACATCTCCCTTCCGAGCAAGAGCTGGCTGAAGCCAAATAACA	780						
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QY	781	TTGCTGCATAGTCTGGGACTCTGGCCCAAGAGCTGTTTCCAGATGAGAAGCTGGAGTAC	840						
Db	1094	TTGCTGCATAGTCTGGGACTCTGGCCCAAGAGCTGTTTCCAGATGAGAAGCTGGAGTAC	1153						
QY	841	ATCCGACAGAGTGTATGTTTCTGACCAATGTGAACAGCTCCAGCTCCACCCAAATC	900						
Db	1154	ATCCGACAGAGTGTATGTTTCTGACCAATGTGAACAGCTCCAGCTCCACCCAAATC	1213						
QY	901	TACCAGGCTGTGCTCGTATTGTCTGGGCAATCCCGAGGAGGGGGCTGAAGATCAAG	960						
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Db	1454	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGSCAGGTCATGGCTGAGTGAAC	1513						
QY	1201	AAGACCTTCCAGGAATGGCTGTGTTCATGATCTGGAAGCATGTGGAGGAATCAGC	1260						
Db	1514	AAGACCTTCCAGGAATGGCTGTGTTCATGATCTGGAAGCATGTGGAGGAATCAGC	1573						
QY	1261	CCCAAGATCTGGACCTTTCATGAGAACCAAGAAATGGACCTTGTCCGATGCTGTG	1320						
Db	1574	CCCAAGATCTGGACCTTTCATGAGAACCAAGAAATGGACCTTGTCCGATGCTGTG	1633						
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QY	1381	CAAGACATCGTGGCGCTTTTGGCCAAAGCAACCCAGAGGATGCCAGTCCAGTAATGGTCT	1440						
Db	1694	CAAGACATCGTGGCGCTTTTGGCCAAAGCAACCCAGAGGATGCCAGTCCAGTAATGGTCT	1753						
QY	1441	GTGTACACTGGAGAGAGCTTTCAACGAGACTAACACAGGCAATCCGACCATATCTCGC	1500						
Db	1754	GTGTACACTGGAGAGAGCTTTCAACGAGACTAACACAGGCAATCCGACCATATCTCGC	1813						
QY	1501	TTTATGGAGTGTCTCAACTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1560						
Db	1814	TTTATGGAGTGTCTCAACTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1873						
QY	1561	AAACAAGTCCATGAGCTGCTGGATGAGAGGAGTTCTGGCTGGTATTGTGTTCACTGGA	1620						
Db	1874	AAACAAGTCCATGAGCTGCTGGATGAGAGGAGTTCTGGCTGGTATTGTGTTCACTGGA	1933						
QY	1621	ATTACTCCAGGACGATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1680						
Db	1934	ATTACTCCAGGACGATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1993						
QY	1681	GACAAATGGAGAGGACAAATAAATCAAGATGGTACTGGGACCCCTGGCTCGAGCT	1740						
Db	1994	GACAAATGGAGAGGACAAATAAATCAAGATGGTACTGGGACCCCTGGCTCGAGCT	2053						
QY	1741	GACCCCTTTGAGGACATCGGTACGTCTGGGGGGCTTTCGCTACTTGCAGGATGGTG	1800						
Db	2054	GACCCCTTTGAGGACATCGGTACGTCTGGGGGGCTTTCGCTACTTGCAGGATGGTG	2113						
QY	1801	GAGCAGCAATCATCAGGCTGCTGACGGCCACCGAGAGAAACTGGTGTCTATATGCAA	1860						
Db	2114	GAGCAGCAATCATCAGGCTGCTGACGGCCACCGAGAGAAACTGGTGTCTATATGCAA	2173						
QY	1861	CAGATGCCCTATCCCTGTTTACGTTCATGACATCTTTCTCGGGGTGATGAGCCGGTCAATG	1920						
Db	2174	CAGATGCCCTATCCCTGTTTACGTTCATGACATCTTTCTCGGGGTGATGAGCCGGTCAATG	2233						
QY	1921	CCCTCTTCATGACCGTGGCTTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1980						
Db	2234	CCCTCTTCATGACCGTGGCTTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	2293						
QY	1981	TATGAGAAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTTGACAAACAGCATA	2040						
Db	2294	TATGAGAAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTTGACAAACAGCATA	2353						
QY	2041	CTCTGGTTTACGTGGTTCATTAAGTAGCCTCATCTCTTCTTTGTGAGCGCTGGCTGCTA	2100						
Db	2354	CTCTGGTTTACGTGGTTCATTAAGTAGCCTCATCTCTTCTTTGTGAGCGCTGGCTGCTA	2413						
QY	2101	GTGGTCACTCTCAAGTTAGGAACCTGCTGCCCTACAGTATCCAGCGGTGGTGTGTC	2160						

Db 2414 GTGGTCATCCTGAAGTTAGGAACCTGCTGCGCCCTACAGTATCCAGCGTGGTGTTC 2473
QY 2161 TTCCTGTCGGTGTTCCTGCTGTGTGACAACTCCCTGACAGTGTTCCTGATTAGCACACTTC 2220
Db 2474 TTCCTGTCGGTGTTCCTGCTGTGTGACAACTCCCTGACAGTGTTCCTGATTAGCACACTTC 2533
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Db 2594 TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTTCACACTCAAGATCTTCCCTAGC 2653
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Db 2774 CTCACACTTCGATCTCCATGATGCTGTTGACACCTTCTCTATGGGAGTATGACCTGG 2833
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Db 3494 GCTGTGTGGACCTTACTCCCGAGGGGAATATGGGAGCTGTGCTGCTGAATATCCGACAA 3553

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Qy 6781 GTAT GTAT 6784
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; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFILE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
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; SEQ ID NO 121
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c o r g
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QY	301	ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTTCTTTATACAGCAGAAAGACACC	360
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QY	361	AGCATGAAGGACATGCGCAAGTCTTGAGAACATTACAGCAGATCAAGAAATCCAGTCA	420
Db	674	AGCATGAAGGACATGCGCAAGTCTTGAGAACATTACAGCAGATCAAGAAATCCAGTCA	733
QY	421	AAC TTGAAGCTTCAAGATTTCCTGGTGGACAATGAACCTCTCTGGGTTCCTATATCAC	480
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QY	481	AACCTCTCTCCCAAAGTCTACTGGACAAGATGCTGAGGCGTGATGTCAATTCAC	540
Db	794	AACCTCTCTCCCAAAGTCTACTGGACAAGATGCTGAGGCGTGATGTCAATTCAC	853
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QY	601	GAAGAGATGATTAAC TTGGTGACCAAGATTTCTGAGCTTTTGTGGCTACCAAGAGG	660
Db	914	GAAGAGATGATTAAC TTGGTGACCAAGATTTCTGAGCTTTTGTGGCTACCAAGAGG	973
QY	661	AAATGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCTGT	720
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QY	721	AGACACTAAACTCTACATCTCCCTCCCGACGAGGAGCTGGCTGAAGCCACAAAACA	780
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QY	781	TTGTGCTATAGCTTGGGACTCTGGGCCACGAGGAGCTGTTCAAGATCAGAGCTGGAGTGAC	840
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QY	961	TCTCTCAACTGGTATGAGGACACAACTACAAGGCCCTTTTGAGGCAATGGGCACGTGAG	1020
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QY	1141	GGGAAGATCTGTATACAGCTGACACTCCAGCCACAAGCAGGTCAATGGCTGAGGTGAAC	1200
Db	1454	GGGAAGATCTGTATACAGCTGACACTCCAGCCACAAGCAGGTCAATGGCTGAGGTGAAC	1513
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QY	1261	CCCAAGATCTGGACCTTCATGGAAGAACACGCCAAGAAATGGACCTTGTCCGGATGCTGTG	1320
Db	1574	CCCAAGATCTGGACCTTCATGGAAGAACACGCCAAGAAATGGACCTTGTCCGGATGCTGTG	1633

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QY	1381	CAGACATCGTGGCGTTTGGSCAAGCACCCACAGAGATGTCAGTCCAGTAATGTTCT	1440
Db	1694	CAGACATCGTGGCGTTTGGSCAAGCACCCACAGAGATGTCAGTCCAGTAATGTTCT	1753
QY	1441	GTGTACACCTGGAGAGAAGCTTTCACGAGACTAACCAGGCAATCCGGACCATATCTCG	1500
Db	1754	GTGTACACCTGGAGAGAAGCTTTCACGAGACTAACCAGGCAATCCGGACCATATCTCG	1813
QY	1501	TTCATGGAGTGTCAACCTGNACAAGCTAGAACCCATACACAGAAAGTCTGGCTCATC	1560
Db	1814	TTCATGGAGTGTCAACCTGNACAAGCTAGAACCCATACACAGAAAGTCTGGCTCATC	1873
QY	1561	AACAAGTCCATGGAGCTGTGTGATCAGAGGAAGTCTTGGGTGTGATGTGTTCACTGGA	1620
Db	1874	AACAAGTCCATGGAGCTGTGTGATCAGAGGAAGTCTTGGGTGTGATGTGTTCACTGGA	1933
QY	1621	ATTACTCCAGGACGATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1680
Db	1934	ATTACTCCAGGACGATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1993
QY	1681	GACAATGTGGAGGACAAATAAATCAAGGATGGTACTGGGACCTGGCTCGTAGCT	1740
Db	1994	GACAATGTGGAGGACAAATAAATCAAGGATGGTACTGGGACCTGGCTCGTAGCT	2053
QY	1741	GACCCCTTTGAGACATGCGGTACGCTGTGGGGGGCTTCGCCCTACTTGCAGATGTGGTG	1800
Db	2054	GACCCCTTTGAGACATGCGGTACGCTGTGGGGGGCTTCGCCCTACTTGCAGATGTGGTG	2113
QY	1801	GACGAGCAATCATCAGGCTGCTGACGGGCACCGAGAGAAACTGGTGCTATATGCAA	1860
Db	2114	GACGAGCAATCATCAGGCTGCTGACGGGCACCGAGAGAAACTGGTGCTATATGCAA	2173
QY	1861	CAGATGCCCTATCCCTGTACCTTGTGATGACATCTTCTGCGGGTGATGACCGGCTCAATG	1920
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QY	1921	CCCTCTTTCATGACGCTGGCGCTGGATTACTCAGTGGCTGTGATCATCAGGGGCACTGGT	1980
Db	2234	CCCTCTTTCATGACGCTGGCGCTGGATTACTCAGTGGCTGTGATCATCAGGGGCACTGGT	2293
QY	1981	TATGAGAAGGAGCAGCGCTGAAAGAGACCATGCGGATCATGGGCCTGGACACAGCAT	2040
Db	2294	TATGAGAAGGAGCAGCGCTGAAAGAGACCATGCGGATCATGGGCCTGGACACAGCAT	2353
QY	2041	CTCTGGTTTACGTGGTTCAITTAGTAGCCCTCATCTCCTCTTCTGTGAGCGCTGGCCTGCT	2100
Db	2354	CTCTGGTTTACGTGGTTCAITTAGTAGCCCTCATCTCCTCTTCTGTGAGCGCTGGCCTGCT	2413
QY	2101	GTGTCATCTCGAAGTTAGGAACCTGCTGCCCTACAGTGATCCACAGCTGGTGTGTTGTC	2160
Db	2414	GTGTCATCTCGAAGTTAGGAACCTGCTGCCCTACAGTGATCCACAGCTGGTGTGTTGTC	2473
QY	2161	TTCCTGTCCGTGTTTCTGTGTGACATCTCTGACGTGCTTCTCTGATTTAGCACACTCTTC	2220
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Db	2534	TCCAGAGCCAACTGGCAGCAGCTGTGGGGGCATCATCTACTTCACGCTGACTCGCC	2593
QY	2281	TAGTCTCTGTGTGTGCGATGGCAGGACTACGTGGGGCTTCACATCAAGATCTCGCTAGC	2340
Db	2594	TAGTCTCTGTGTGTGCGATGGCAGGACTACGTGGGGCTTCACATCAAGATCTCGCTAGC	2653
QY	2341	CTGCTGTCTCCTGTGGCTTTTGGTGTGACTGTGAGTACTTTGCCCTTTTGTGAGAGCAG	2400
Db	2654	CTGCTGTCTCCTGTGGCTTTTGGTGTGACTGTGAGTACTTTGCCCTTTTGTGAGAGCAG	2713
QY	2401	GGCAITGGAGTGCAGTGGGACACACCTGTTTGGAGTCTCTGTGGAGAGAGATGGCTTCAAT	2460

Db	2714	GGCATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTTCAAT	2773
Qy	2461	CTCACCACATTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATCACTGG	2520
Db	2774	CTCACCACATTCGCTCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATCACTGG	2833
Qy	2521	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCTCTTGC	2580
Db	2834	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCTCTTGC	2893
Qy	2581	ACCAAGTCTACTGTTTGGCGAGGAAAGTGATGAGAGAGCCACCCTGGTCTCCAAACCAG	2640
Db	2894	ACCAAGTCTACTGTTTGGCGAGGAAAGTGATGAGAGAGCCACCCTGGTCTCCAAACCAG	2953
Qy	2641	AAGAGAAATGTCAGAAATCTGCATGGAGGAGGAACCCACCCACTTTGAAGCTGGGGGTGTC	2700
Db	2954	AAGAGAAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTTGAAGCTGGGGGTGTC	3013
Qy	2701	ATTTCAGAACTGTTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCTGGCA	2760
Db	3014	ATTTCAGAACTGTTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCTGGCA	3073
Qy	2761	CTGAAATTTTATGAGGGCCAGATCACTCTCTCTGGGCCACAATGAGAGCGGGGAAGCG	2820
Db	3074	CTGAAATTTTATGAGGGCCAGATCACTCTCTCTGGGCCACAATGAGAGCGGGGAAGCG	3133
Qy	2821	ACCACCATGTCATCTGACCGGGTGTTCCTCCCGACCTCGGCGACCGCTACATCTTG	2880
Db	3134	ACCACCATGTCATCTGACCGGGTGTTCCTCCCGACCTCGGCGACCGCTACATCTTG	3193
Qy	2881	GGAAAAGACATTCGCTCTGAGATGAGCACCATTCGGCGAGAACCTTGGGGTCTGTCCCCAG	2940
Db	3194	GGAAAAGACATTCGCTCTGAGATGAGCACCATTCGGCGAGAACCTTGGGGTCTGTCCCCAG	3253
Qy	2941	CATAAGTGTCTGTTTGACATGCTGACTCTCGAGAGACACATCTGGTCTATGCCCGTTCG	3000
Db	3254	CATAAGTGTCTGTTTGACATGCTGACTCTCGAGAGACACATCTGGTCTATGCCCGTTCG	3313
Qy	3001	AAAGGGCTCTCTGAGAAGCACGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT	3060
Db	3314	AAAGGGCTCTCTGAGAAGCACGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT	3373
Qy	3061	TTGCCATCAAGCAAGCTGAAAAGCAAAACACCCAGCTGTCTAGTGGNAATCGACAGAAG	3120
Db	3374	TTGCCATCAAGCAAGCTGAAAAGCAAAACACCCAGCTGTCTAGTGGNAATCGACAGAAG	3433
Qy	3121	CTATCTGTGCCCTTGGCCTTTGCGGGGATCTAAGTGTTCATCTGGATGAACCCACA	3180
Db	3434	CTATCTGTGCCCTTGGCCTTTGCGGGGATCTAAGTGTTCATCTGGATGAACCCACA	3493
Qy	3181	GCTGGTGTGACCCCTTACTCCCGACGGGAATATGGGAGCTGTCTGTAATACCGACAA	3240
Db	3494	GCTGGTGTGACCCCTTACTCCCGACGGGAATATGGGAGCTGTCTGTAATACCGACAA	3553
Qy	3241	GGCCGACCAATTATCTCTACACACACATGATGAAGCGGAGCTCTGGGGACAGG	3300
Db	3554	GGCCGACCAATTATCTCTACACACACATGATGAAGCGGAGCTCTGGGGACAGG	3613
Qy	3301	ATTGCCATCATCTCCCATGGGAAGCTGTCTGTGTGGGCTCTCCCTGTTTCTGAAGAAC	3360
Db	3614	ATTGCCATCATCTCCCATGGGAAGCTGTCTGTGTGGGCTCTCCCTGTTTCTGAAGAAC	3673
Qy	3361	CAGCTGGGAACAGCTTACTCTGACCTTGGTCAAGAAAGATGGAATCTCTCCCTCAGT	3420
Db	3674	CAGCTGGGAACAGCTTACTCTGACCTTGGTCAAGAAAGATGGAATCTCTCCCTCAGT	3733
Qy	3421	TCTTCGAGAAACAGTAGTACAGTGTCTATACCTGAAAAGGAGGACAGTGTCTTCAG	3480
Db	3734	TCTTCGAGAAACAGTAGTACAGTGTCTATACCTGAAAAGGAGGACAGTGTCTTCAG	3793
Qy	3481	AGCAGTTCTGATGTTGGCTGGCAGCGACCATGAGAGTGACACCTGACCATCGATGTC	3540

Db 3794 AGCAGTTCTGATGCTGGCCCTGGCAGCGACCATTGAGAGTGACACGGTGACCATCGATGTC 3853
Qy 3541 TCTGCTATCTCCAACTCATCAGGAGCATGTGCTGAGACCCGGCTGGTGAACACATA 3600
Db 3854 TCTGCTATCTCCAACTCATCAGGAGCATGTGCTGAGACCCGGCTGGTGAACACATA 3913
Qy 3601 GGCATGAGCTGACCTATGCTGCTGATGATGAGCTGCTGAGGAGGAGCCCTTTGTGAA 3660
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Qy 3661 CTTCTTCATGAGATTGATGAGCGGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 3720
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Qy 3721 GAGACGACCTTGAAGAAATATTCTCAAGTGGCGGAGAGAGTGGGTGATGCTGAG 3780
Db 4034 GAGACGACCTTGAAGAAATATTCTCAAGTGGCGGAGAGAGTGGGTGATGCTGAG 4093
Qy 3781 ACCTCAGATGGTACCTTGCAGCAAGACAGGCGGCGCTTCGGGACAGCAGAGC 3840
Db 4094 ACCTCAGATGGTACCTTGCAGCAAGACAGGCGGCGCTTCGGGACAGCAGAGC 4153
Qy 3841 TGTCTTCGCGCGCTTCACTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 3900
Db 4154 TGTCTTCGCGCGCTTCACTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 4213
Qy 3901 GAATCAGAGACAGACTGCTCAGTGGGATGATGCAAGGCTCCTACAGGTGAAA 3960
Db 4214 GAATCAGAGACAGACTGCTCAGTGGGATGATGCAAGGCTCCTACAGGTGAAA 4273
Qy 3961 GCGTGAACCTTACACAGCAAGAGTTGTGGCCCTTTGTGGAAGAGAGCTGAATGCCC 4020
Db 4274 GCGTGAACCTTACACAGCAAGAGTTGTGGCCCTTTGTGGAAGAGAGCTGAATGCCC 4333
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Db 4574 GGAACCCAAATCCACAGACACGCTTCCAGGAGGAGAGTGGACCACTGCCCA 4633
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Db 4634 GTTCCAGACCATCATGGACCTCTTCCAGAAATGGAACTGGCAATGCAAGACCCCTTCA 4693
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Qy 4441 GCAGGGGGCTGCTCCTCCCAAGAAACAAACACTGCAGATATCCTTCAGGACCTG 4500
Db 4754 GCAGGGGGCTGCTCCTCCCAAGAAACAAACACTGCAGATATCCTTCAGGACCTG 4813
Qy 4501 ACAGGAACAAACATTTCCGATTATCTGTGAGACGATGTCAGATCATAGCCAAAGC 4560
Db 4814 ACAGGAACAAACATTTCCGATTATCTGTGAGACGATGTCAGATCATAGCCAAAGC 4873
Qy 4561 TTAAGAACAAAGATCTGGGTGAATGAGTTTATGATGCGGCTTTTCCCTGGGTGTCAGT 4620
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Qy 4681 CACCTAAAGCTGGCCAAAGCAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT 4740
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Qy 5521 GTCTACCATTAATCTTGGGACTTGGTGGGACGAAACCTCTTCCCATGCCCCTGGAAGGG 5580
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DB 6194 GGAGATACACATGTTACAGAGAGATGCTTTCCTTACAAATAGTATCTTATCAAC 6253
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DB 7094 GTAT 7097
RESULT 14
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; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-122
Query Match 99.7%; Score 5764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 181 ATGCCCTCTGCAGGAACACTTCTTGGGTTCAGGGGATTTATCTGTAATGCCAAACACCC 240
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 Db 4814 ACAGAAAGAAACATTTCCGATTTCTGGTGAAGACGTATGTGCAGATCATAGCCAAAGC 4873
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RESULT 15
 US-09-595-526c-123
 ; Sequence 123, Application US/09984827
 ; Publication No. US20030056234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEFFLE, PATRICE
 ; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
 ; APPLICANT: ARNOULD-REGUINE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
 ; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984.827
 ; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 123
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-123

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
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Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 1861 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTTCGCGGTGATGAGCCGTTCAATG 1920

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QY 6781 GTAT 6784
Db 7094 GTAT 7097

Search completed: April 4, 2003, 06:45:44
Job time : 505.143 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 3, 2003, 09:40:44 ; Search time 7668.53 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526c-l_COPY_291_7074
Perfect score: 6784
Sequence: 1 atgctttgttgctcagct.....agtgaagaagaagctatgtat 6784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vit:*
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23: em_gss_mam:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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2	639.8	9.4	854 13	BI854140
3	543.6	8.0	837 12	BF160011
4	536.8	7.9	652 10	BB468374
5	532.4	7.8	724 13	BG920223
6	526.6	7.8	720 13	BI248317

7	508.2	7.5	702	13	BI658600
8	483.6	7.1	1004	11	BC034824
9	474.6	7.0	878	13	BI182779
10	473	7.0	562	10	BE65489
11	459.4	6.8	515	12	BF04524
12	447.6	6.6	554	12	BF076322
13	433.2	6.4	518	12	BF042703
14	428.8	6.3	463	12	BF15104
15	425.4	6.3	427	13	BM153383
16	424.2	6.3	998	12	RG678861
17	411	6.1	596	9	AA063753
18	399.2	5.9	417	10	AA062709
19	366.2	5.4	412	10	AW380897
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23	362	5.3	422	12	BE929660
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25	340.8	5.0	717	12	BE742059
26	337	5.0	835	10	AW013420
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28	325.8	4.8	623	10	AW421371
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36	309	4.6	641	14	BQ637544
37	308.8	4.6	381	12	BE757461
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ALIGNMENTS

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DEFINITION mRNA sequence.
ACCESSION BI754756
VERSION BI754756.1 GI:15746334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 809)
NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
UNPUBLISHED (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM1490 row: i column: 20
High quality sequence stop: 768.

FEATURES
Source Location/Qualifiers
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QY 6289 GTAGTGTATACATCTCATAGTATGGAAGATGTGAAGCTCTTTGCACTAGATGCGCAATC 6348
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mRNA sequence.
BF160011
BF160011.1 GI:11040118
EST.
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9194 row: g column: 24
High quality sequence stop: 669.
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FEATURES
source

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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 226 a 188 c 230 g 193 t
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Matches 647; Conservative 0; Mismatches 79; Indels 6; Gaps 5;
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QY 6322 GAAGCTCTTTCACATAGGATGCAATCATGTCATAGGAAGTTTCAGTGCCTTGGCAGT 6381
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QY 6502 CTAAGAGAGAAACACCGGCAACATGCTACAAATACCAGCTTCCATCTCATATCTTCTCTG 6561
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QY 6681 TGACCACCTTAAA 6692
Db 729 TTGACCTTTAAA 740

RESULT 4
B3468374
LOCUS
DEFINITION
BB468374 RIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230019D04 3' similar to X75926 M.musculus abcl
mRNA. mRNA sequence.
ACCESSION
VERSION
KEYWORDS
BB468374
BB468374.2 GI:16427507
EST.

SOURCE
ORGANISMhouse musculus
Mus musculusREFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 652)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
COMMENT

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jul 22, 2000 this sequence version replaced gi:9385563.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakawa, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source

Location/Qualifiers
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/tissue_type="eyeball"
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/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by

cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGTGATTAATAATAATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

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ORIGIN

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Matches 580; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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724 bp mRNA linear EST 05-JUN-2001
mRNA sequence.

ACCESSION Bg920223.1 GI:14300699

VERSION Bg920223

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 724)

NTN-MGC http://mnc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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ACCESSION	BI248317			
VERSION	BI248317.1	GI:14794093		
KEYWORDS	EST.			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
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REFERENCE	1 (bases 1 to 720)			
AUTHORS	NH-MGC			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			

JOURNAL COMMENT
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbsr@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: In Vitro Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11283 Row: d Column: 06
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Library constructed by Life Technologies. Investigator
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BASE COUNT
ORIGIN

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ACCESSION BI658600
VERSION BI658600.1 GI:15572836
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11833 row: f column: 09
High quality sequence stop: 645.
Location/Qualifiers
1. :702
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5328392"
/clone_lib="NCI_CGAP_Mam4"

FEATURES
source
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: Mammary; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
```

```

BASE COUNT 191 a 166 c 172 g 173 t
ORIGIN
Query Match 7.5%; Score 508.2; DB 13; Length 702;
Best Local Similarity 91.8%; Pred. No. 5e-128;
Matches 548; Conservative 0; Mismatches 48; Indels 1; Gaps 1;
QY 6189 TCCTGTGTGTTCTTGGATGAACCCACACAGGATGATCCCAAGCCGCGGTCTTT 6248
Db 1 TCCTGTGTGTTCTTGGATGAACCCACACAGGATGATCCCAAGCCGCGGTCTTT 60
QY 6249 GTGGAATGTGCTTAACTGTGTCAAGGAGGGAGATCAGTGTCTTACATCTCATAG 6308
Db 61 GTGGAATGTGCTTAACTGTGTCAAGGAGGGAGATCAGTGTCTTACATCTCATAG 120
QY 6309 TATGGAAGATGTGAAGCTCTTTCGACTAGGATGCAATCATGTGTAAGGTTTCTAG 6368
Db 121 TATGGAAGATGTGAAGCTCTTTCGACTAGGATGCAATCATGTGTAAGGTTTCTAG 180
QY 6369 GTGCTTGGCAGTGTCCAGCATCTTAAAGATAGTTTGGAGATGTTTATACATAGTTGT 6428
Db 181 GTGCTTGGCAGTGTCCAGCATCTTAAAGATAGTTTGGAGATGTTTATACATAGTTGT 240
QY 6429 ACATATAGCAGGTTCCAAACCGGACCTGAGCCTGTCCAGGATTTCTTGGACTTGCAT 6488
Db 241 ACATATAGCAGGTTCCAAACCGGACCTGAGCCTGTCCAGGATTTCTTGGACTTGCAT 300
QY 6489 TCCTGGAAGTGTCTTAAAGAGAAACACCGGAAACATGCTACATACCACTTCCATCTTC 6548
Db 301 TCCTGGAAGTGTCTTAAAGAGAAACATGCTACATACCACTTCCATCTTCATCTTC 360
QY 6549 ATTATCTTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAGGACTTCCACAT 6608
Db 361 CTGTGTCATCTCTAGCCAGGATATTCAGCATCTCTCCAGAGCAAAAGGACTTCCACAT 420
QY 6609 AGAGACTACTCTGTTTCTCAGACAACTTGTGCAAGTATTTGTGAATTTGCCAAGGA 6668
Db 421 AGAGACTACTCTGTTTCTCAGACAACTTGTGCAAGTATTTGTGAATTTGCCAAGGA 480
QY 6669 CCAAGTGTATGATCACCACCTTAAAGAGACCTCTCATTTACAAAAACACAGACAGTAGTGA 6728
Db 481 CCAAGTGTATGATCACCACCTTAAAGAGACCTCTCATTTACAAAAACACAGACAGTAGTGA 540
QY 6729 CGTTGAGTTCTCAGATCTTTTCTACAGGATGA-GAAAGTGAAGAAAGTATGTAT 6784
Db 541 TGTGCGCGTTCTCAGATCTTTTCTACAGGATGAAGGACCTGACAGAAAGTCAATGTAT 597

RESULT 8
BC034824
LOCUS BC034824 Homo sapiens, clone IMAGE:4749735, mRNA.
DEFINITION BC034824
ACCESSION BC034824
VERSION BC034824.1 GI:21961568
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 1004) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
```

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: angbcm.tmc.edu
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK File: 52 Row: d Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5915657
This clone has the following problem: incomplete processing.

FEATURES
Location/Qualifiers
1..1004
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4749735"
/tissue_type="Skin, squamous cell carcinoma"
/clone_lib="NCI CGAP_Skn4"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6.cdb"
306 a 234 c 230 g 234 t

BASE COUNT
ORIGIN
Query Match 7.1%; Score 483.6; DB 11; Length 1004;
Best Local Similarity 96.3%; Pred. No. 4.1e-121;
Matches 495; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 33 GTGGAAGACCTCAGTTTCAGAGAGACAAACATGTACGCTGTTACTGGAATGGCCCTG 92
DB 172 GAGAAAGAGACGCAACACAAAGAGTGAACAGTGTACGCTGCTGGAATGGCCCTG 231
QY 93 GCCTCTATTATCTCTGATCTCTGATCTGTTGCTGCTGAGTACCCACCTATCAACA 152
DB 232 GCCTCTATTATCTCTGATCTCTGATCTGTTGCTGCTGAGTACCCACCTATCAACA 291
QY 153 ACATGAATGCCATTTTCCAAATTAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTCA 212
DB 292 ACATGAATGCCATTTTCCAAATTAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTCA 351
QY 213 GGGGATTATCTGTAATGCCAACACCCCTGTTCCCTTACCCGACTCCTGGGAGGCTCC 272
DB 352 GGGGATTATCTGTAATGCCAACACCCCTGTTCCCTTACCCGACTCCTGGGAGGCTCC 411
QY 273 CGGAGTTGTTGGAACATTTAACAAATCCATTTGTCGCTGCTTCTCAGATGCTCGGAG 332
DB 412 CGGAGTTGTTGGAACATTTAACAAATCCATTTGTCGCTGCTTCTCAGATGCTCGGAG 471
QY 333 GCCTCTTTTATACAGCCAGAAACACACAGCAGTACGAGGACATCGGCAAGTTCTGAGAAC 392
DB 472 GCCTCTTTTATACAGCCAGAAACACACAGCAGTACGAGGACATCGGCAAGTTCTGAGAAC 531
QY 393 ATTACAGCAGATCAAGAAATCCAGCTCAAACTTGAAGCTTCAAGATTCTCGTGGTGACAA 452
DB 532 ATTACAGCAGATCAAGAAATCCAGCTCAAACTTGAAGCTTCAAGATTCTCGTGGTGACAA 591
QY 453 TGAACCTTCTCTGGGTTCTATATACACACCTCTCTCTCCCAAGTCTACTGTGGACAA 512
DB 592 TGAACCTTCTCTGGGTTCTATATACACACCTCTCTCTCCCAAGTCTACTGTGGACAA 651
QY 513 GATCGTCAGGGCTGATCTATCTTCCACAGGTA 546
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Db 652 GATGCTGAGGGCTGATGTCTTCATCTCCACAAGGTA 685

RESULT 9
B1182779/c
LOCUS
DEFINITION
B1182779 878 bp mRNA linear EST 10-JUL-2001
UNL-P-FN-bp-c-01-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-bp-c-01-0-UNL 3', mRNA sequence.
ACCESSION
B1182779
VERSION
B1182779.1 GI:14657188
KEYWORDS
EST.
SOURCE
Sus scrofa pig.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 878)
Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
Unpublished (2001)
JOURNAL
COMMENT
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail.
Seq primer: M13 -29
POLYA=yes.
Location/Qualifiers
1..878
/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-bp-c-01-0-UNL"
/clone_lib="UNL-P-FN"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT3p-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
1996.
TAG_SEQ=None found"
BASE COUNT 212 a 219 c 184 g 258 t 5 others
ORIGIN
Query Match 7.0%; Score 474.6; DB 13; Length 878;
Best Local Similarity 89.6%; Pred. No. 1.1e-118;
Matches 533; Conservative 0; Mismatches 59; Indels 3; Gaps 2;

QY 6190 CCTGTGGTCTTCTGATGAACCCACACAGGATGGATCCCAAGCCCGCGGTTCTTG 6249
DB 771 CCCCTGTGCTTCTGATGAACCCACACAGGAT-GATCCCAAGCCCGCGGATCT-- 715
QY 6250 TGAATTTGCCCTTAAGTGTTCAGAGAGGGAGATCAGTAGTGTTCATCTCATAGT 6309
DB 714 GTGAATTTGCCCTTAAGTGTTCAGAGAGGGAGATCAGTAGTGTTCATCTCATAGT 655
QY 6310 ATGGAAGATGTGAAGCTCTTTGCACTAGGATGGCAATCATGTCAATGAAGGTTTCAG 6369
DB 654 ATGGAAGATGTGAAGCTCTTTGCACTAGGATGGCAATCATGTCAATGAAGGTTTCAG 595
|||||

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR0-UT0047-170
900-202-f10&t3=2000-09-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 515.

FEATURES
Source
1..515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0047"
/dev_stage="Adult"
/note="Organ: uterus; tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 143 a 125 c 132 g 115 t
ORIGIN
Query Match 6.8%; Score 459.4; DB 12; Length 515;
Best Local Similarity 98.4%; Pred. No. 1.1e-114;
Matches 485; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY 1049 CTCAACTCCTTACTGCAATGATTGATGAAGATTGGAGTCTAGTCCCTTTCCGCGA 1108
Db 15 CTCAACTCCTTACTGCAATGATTGATGAAGATTGGAGTCTAGTCCCTTTCCGCGA 74
QY 1109 TTATCTGGAAAGCTCTGAAGCGCTGCTGCTGGGAAGATCTCTATACACCTGACACTC 1168
Db 75 TTATCTGGAAAGCTCTGAAGCGCTGCTGCTGGGAAGATCTCTATACACCTGACACTC 134
QY 1169 CAGCCACAGGCGATGCTGCTGAGTGACAGACCTTCCAGAGACTGCTGTGTCC 1228
Db 135 CAGCCACAGGCGATGCTGCTGAGTGACAGACCTTCCAGAGACTGCTGTGTCC 194
QY 1229 ATGATCTGGAAAGCATGTGGGAGGAATCAGCCCAAGATCTGGACCTTCATGGAGAAC 1288
Db 195 ATGATCTGGAAAGCATGTGGGAGGAATCAGCCCAAGATCTGGACCTTCATGGAGAAC 254
QY 1289 GCCAAGAAATGACCTGTGTCGGATGCTGTGGACAGGAGCAATGACCACTTTTGGG 1348
Db 255 GCCAAGAAATGACCTGTGTCGGATGCTGTGGACAGGAGCAATGACCACTTTTGGG 314
QY 1349 AACAGCAGTTGGATGGCTTAGATTGGACAGCCCAAGACATCGTGGCGTTTGGCCCAAGC 1408
Db 315 AACAGCAGTTGGATGGCTTAGATTGGACAGCCCAAGACATCGTGGCGTTTGGCCCAAGC 374
QY 1409 ACCCAGAGGATGTCCAGTCCAGTAAATGTTCTGTACACCTGAGAGAGCACTTCAACG 1468
Db 375 ACCCAGAGGATGTCCAGTCCAGTAAATGTTCTGTACACCTGAGAGAGCACTTCAACG 434
QY 1469 AGACTTAA-CCAGGAATCCGACCATATCTCGCTTCATGGAGTGTGTAACCTGAACAAG 1527
Db 435 AGACTTAA-CCAGGAATCCGACCATATCTCGCTTCATGGAGTGTGTAAC-CTGAACAAG 493
QY 1528 CTAGAACCCTAG 1540
Db 494 CTAGAACCCTAG 506
RESULT 12

BF076322
LOCUS 225856 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
DEFINITION BF076322
ACCESSION BF076322
VERSION BF076322.1 GI:10870075
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 554)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G.,
Perte, G., Holt, I., Karameycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 86 row: N column: 9
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Source
1..554
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 138 a 146 c 146 g 124 t
ORIGIN
Query Match 6.6%; Score 447.6; DB 12; Length 554;
Best Local Similarity 89.2%; Pred. No. 2.1e-111;
Matches 494; Conservative 0; Mismatches 59; Indels 1; Gaps 1;
QY 774 AAAAATTCCTGCTGATAGTCTTGGACTGTGGCCAGGAGCTGTTGACGATGAGAGCTG 833
Db 1 AAAAGCTTTTGTGATAGTCTTGGATCTGGCCAGAGCTGTTGACGATGAGAGCTG 60
QY 834 GAGTGACATCGACAGGAGGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCCTCCAC 893
Db 61 GAGTGACATCGGAGGAGGTGATGTTCTGACCAAGTGAACAGCTCCAGCTCCTCCAC 120
QY 894 CCAAAATTCACAGCTGTGTCTCGATGTCTGTGCGGCGATCCCGAGGAGGGGGGTGAA 953
Db 121 CCAGATCTACAGGCCCTGTCCCGCATCATCTGCGGCATCCCGAGGCGGGGCGCTGAA 180
QY 954 GATCAAGTCTCAACTGTTATGGGACACACTACAAAGCCCTCTTTTGAGGCAATGG 1013
Db 181 GATCAAGTCTCAACTGTTATGGGACACACTACAAAGCCCTCTTTTGAGGCAATGG 240
QY 1014 CACTGAGGAAGATGCTGAAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTT 1073
Db 241 CACGAGGACGAGCTGSCACCGTCTATGACAACTCTACAACTCTTACTGCAATGATTT 300

QY 1074 GATGAAGAAATTGGAGTCTAGTCTCTCTTCCCGCATATCTGGAAGAGCTCTGAAGCCGCT 1133
 Db 301 GATGAAGAAATTGGAGTCTAGTCTCTCTTCCCGCATATCTGGAAGAGCTCTGAAGCCGCT 360
 QY 1134 GCTGTTGGGAAAGATCTGTATATACCTGACACTCCAGCCACAGGAGGAGTCTGAGTGA 1193
 Db 361 TCTGTTGGGAAAGATCTGTATATACCTGACACTCCAGGAGGAGGAGTCTGAGTGA 420
 QY 1194 GGTGAACAAGACCTTCAGGAA-CTGCTGTGTTCATGATCTGGAAGGAGGATGGGAGG 1252
 Db 421 GGTGAACAAGACCTTCAGGAAAGCTGTGTTCATGATCTGGAAGGAGGATGGGAGG 480
 QY 1253 AACTCAGCCCGACAGCTGACCTTCATGAGAGACAGCCCAAGAAATGGACCTTGTCCGGA 1312
 Db 481 AGCTCAGCCCGACAGCTGACCTTCATGAGAGACAGCCCAAGAAATGGACCTTGTCCGGA 540
 QY 1313 TGTGTTGGGACAGC 1326
 Db 541 CACTGTTGGGACAGC 554

RESULT 13
 LOCUS
 DEFINITION
 BP250020B10D9 Soares normalized bovine placenta Bos taurus cDNA
 clone BP250020B10D9 5', mRNA sequence.

ACCESSION
 BP042703
 VERSION
 BP042703.1 GI:10759758
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE
 AUTHORS
 Lewin,H.A., Soares,M.B., Rebeiz,M., Fardinas,J., Liu,L. and Larson
 J.H.

TITLE
 Bovine ESTs
 Unpublished (2000)

JOURNAL
 COMMENT
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA

Forward: TAATAGCACTCACTATAGG
 BACKWARD: ATTAACTCTCACTAAG
 Insert Length: 518 Std Error: 0.00
 Plate: BP250020B10 row: D column: 9
 Seq primer: AGCGGATAACAATTTTCACACAGGA
 High quality sequence stop: 518.

PCR Primers
 This sequence is vector free and at least 200 bp in length.

Forward: TAATAGCACTCACTATAGG
 BACKWARD: ATTAACTCTCACTAAG
 Insert Length: 518 Std Error: 0.00
 Plate: BP250020B10 row: D column: 9
 Seq primer: AGCGGATAACAATTTTCACACAGGA
 High quality sequence stop: 518.

Location/Qualifiers
 1. 518
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 /db_xref="taxon:9913"
 /clone="BP250020B10D9"
 /clone_lib="Soares normalized bovine placenta"
 /sex="female"
 /lab_host="DH10B"

note="Organ: placenta; Vector: pMT3pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806."

source

BASE COUNT 122 a 121 c 153 g 122 t

Query Match 6.4%; Score 433.2; DB 12; Length 518;
 Best Local Similarity 89.8%; Pred. No. 1.8e-107;
 Matches 465; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1468 GAGACTAAACGAGCAATCGGACCATATCTCGCTTCATGAGTGTGCAACCTGAACAAG 1527
 Db 1 GAGACCAACGAGCAATCGGACCATATCTCGCTTCATGAGTGTGCAACCTGAACAAG 60

QY 1528 CTAGAACCCATAGCAACAGAGTCTGGCTCATCAACAAGTCCATGAGTGTGATGAG 1587
 Db 61 CTAGAACCCATAGCAACAGAGTCTGGCTCATCAACAAGTCCATGAGTGTGATGAG 120

QY 1588 AGGAAGTCTGGGCTGGTATTGTTCTCACTGGAATTACTCCAGGAGCATTTGAGTGGCC 1647
 Db 121 CGCAATCTGGGCTGGGCTGGTATTGTTCTCACTGGAATTACTCCAGGAGCATTTGAGTGGCC 180

QY 1648 CATCATGTCAAGTACAAGATCCGAATGGACATTTGACATTTGGAGAGCAAAATAAATC 1707
 Db 181 CATCATGTCAAGTACAAGATCCGAATGGACATTTGACATTTGGAGAGCAAAATAAATC 240

QY 1708 AAGGATGGTACTGGGACCCCTGGTCTCGAGTGCACCCCTTTGAGGACATCGGTTACGTC 1767
 Db 241 AAGGATGGTACTGGGACCCCTGGTCTCGAGTGCACCCCTTTGAGGACATCGGTTACGTC 300

QY 1768 TGGGGGGCTTGGCCCTACTTTCAGGATGTGGTGGAGGCAATCATCAGGCTGTGACG 1827
 Db 301 TGGGGGGCTTGGCCCTACTTTCAGGATGTGGTGGAGGCAATCATCAGGCTGTGACG 360

QY 1828 GGCACCGGAGAGAAACCTGGTGTCTATATGCAACAGATGCCCTATCCCTGTTAGCTGTAT 1887
 Db 361 GGCACCGGAGAGAAACCTGGTGTCTATATGCAACAGATGCCCTATCCCTGTTAGCTGTAT 420

QY 1888 GACATCTTCTCGGGGTGATGAGCGGTCATATGCGCCCTTCATGAGCGCTGCCCTGATT 1947
 Db 421 GACATCTTCTCGGGGTGATGAGCGGTCATATGCGCCCTTCATGAGCGCTGCCCTGATT 480

QY 1948 TACTCAGTGGTGTGATCATCAAGGCGATCGTGTATGA 1985
 Db 481 TACTCAGTGGTGTGATCATCAAGGCGATCGTGTATGA 518

RESULT 14
 LOCUS
 DEFINITION
 MR3-HT0737-060700-004-b09 HT0737 Homo sapiens cDNA, mRNA sequence.

ACCESSION
 BE715104
 VERSION
 BE715104.1 GI:10103369
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20020663

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

TITLE
 JOURNAL
 MEDLINE
 COMMENT

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR3-HT0737-060
700-004-B09&t3=2000-07-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 461.

FEATURES

Location/Qualifiers
1..463
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0737"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
147 a 105 c 111 g 100 t

BASE COUNT

Query Match 6.3%; Score 428.8; DB 12; Length 463;
Best Local Similarity 97.3%; Pred. No. 2.7e-106;
Matches 436; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4480 GCAGATATCTTCAGACCTGACAGGAAGAAATTCGGATTATCTGCTGAAGAGCTAT 4539
Db
6 GTAGATATCTTCAGACCTGACAGGAAGAAATTCGGATTATCTGCTGAAGAGCTAT 65
QY 4540 GTCAGATATATGCCAAAGCTTAAAGACAGATCTGGTGAATGAGTTAGGTATGGC 4599
Db
66 GTCAGATATATGCCAAAGCTTAAAGACAGATCTGGTGAATGAGTTAGGTATGGC 125
QY 4600 GGTCTTCCCTGGGTGTCAGTATATCTCAAGCACTTCTCCGAGTCAAGAAGTTAATGAT 4659
Db
126 GGTCTTCCCTGGGTGTCAGTATATCTCAAGCACTTCTCCGAGTCAAGAAGTTAATGAT 185
QY 4660 GGCATCAACAATAGAAACACCTTAAGCTGGCCAAAGACAGTCTCGAGATCGATTT 4719
Db
186 GGCATCAACAATAGAAACACCTTAAGCTGGCCAAAGACAGTCTCGAGATCGATTTA 245
QY 4720 CTCACAGCTTGGAGATTATGACAGGACTGACACAGCAAGTAATATGTCAGAGTGTG 4779
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246 CTCACAGCTTGGAGATTATGACAGGACTGACACAGCAAGTAATATGTCAGAGTGTG 305
QY 4780 TTCAATAACAAGGGTGGCATGCAATCAGCTCTTCTGAAATGTCATCAACAATGCCATT 4839
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QY 4900 CATCCCTGGAATCTCACAAGCAGCAGC 4927
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426 CATCCCTGGAATCTCACAAGCAGCAGC 453

RESULT 15

BM153383
LOCUS
DEFINITION
BM153383 427 bp mRNA linear EST 30-NOV-2001
TCBAP2D11628 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens CDNA clone TCBAP1162, mRNA
sequence.

ACCESSION

BM153383
VERSION
KEYWORDS
SOURCE
EST.
GI:17178477

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 427)
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,
Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric Leukemia CDNA Sequencing Project (2001)
Unpublished (2001)
JOURNAL
COMMENT

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1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@tccc.org

Seq primer:

M13 primer.

Location/Qualifiers

1..427

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="TCBAP1162"

/leukemia_lib="Pediatric pre-B cell acute lymphoblastic

leukemia Baylor-HGSC project=TCBA"

/sex="male"

/tissue_type="leukopheresis"

/cell_type="pre-B cell"

/dev_stage="pediatric 2 years"

/lab_host="DH10B"

/note="vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGAGCTGAGCGCCGAGGAGAG(T)VN
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGGATCGCGCGCAATATAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper..
DNA Res 4: 1, 61-6, Feb 28, 1997")

85 a 104 c 126 g 112 t

BASE COUNT

ORIGIN

Query Match 6.3%; Score 425.4; DB 13; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.2e-105;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1740 TGACCCCTTTGAGGACATCGGTACGCTCTGGGGGGCTTCGCCTACTTCGAGGATGTGT 1799
Db
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QY 1800 GGAGCAGGCAATCATCAGGGTCTGACGGCCACCGAGAGAAACTGGTGCTATATGCA 1859
Db
61 GGAGCAGGCAATCATCAGGGTCTGACGGCCACCGAGAGAAACTGGTGCTATATGCA 120

QY 1860 ACAGATGCCCTATCCCTGTTAGCTTGATGACATCTTCTTCGGGTGATGAGCGGTCAAT 1919
Db
121 ACAGATGCCCTATCCCTGTTAGCTTGATGACATCTTCTTCGGGTGATGAGCGGTCAAT 180

QY 1920 GCCCTCTTCATGACGCTGGCCTGGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCT 1979
Db
181 GCCCTCTTCATGACGCTGGCCTGGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCT 240

QY 1980 GTATGAGAGGAGGACGCGCTGAAAGAGACCATGCGGATCATGGGCTCGACAAACAGCAT 2039
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QY 2040 ACTCTGGTTAGCTGTTTCATAGTAGCCTCATTCCTCTTGTGAGCGCTGGCCTGCT 2099
Db
301 CCTCTGTTAGCTGTTTCATAGTAGCCTCATTCCTCTTGTGAGCGCTGGCCTGCT 360

QY 2100 AGTGGTCATCCTGAAGTATAGGAAACCTGCTGCCCTACAGTATCCCGAGCGTGTGTTTCT 2159

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Db 361 AGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCAGCGTGGTGTGT 420
QY 2160 CTTCCCTG 2166
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Db 421 CTTCCCTG 427

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Job time : 7723.53 secs